

Match length 122
 % identity 87
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 398082
 Seq. ID LIB3431-010-P1-K1-G8
 Method BLASTX
 NCBI GI g115796
 BLAST score 737
 E value 2.0e-78
 Match length 148
 % identity 96
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi_218174_dbj_BAA00537_ (D00642) type II light-harvesting chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 398083
 Seq. ID LIB3431-010-P1-K1-G9
 Method BLASTX
 NCBI GI g2737973
 BLAST score 742
 E value 5.0e-79
 Match length 145
 % identity 96
 NCBI Description (U83625) protein kinase ZmMEK1 [Zea mays]

Seq. No. 398084
 Seq. ID LIB3431-010-P1-K1-H10
 Method BLASTX
 NCBI GI g3551523
 BLAST score 247
 E value 6.0e-21
 Match length 156
 % identity 37
 NCBI Description (AB017026) oxysterol-binding protein [Mus musculus]

Seq. No. 398085
 Seq. ID LIB3431-010-P1-K1-H11
 Method BLASTX
 NCBI GI g231610
 BLAST score 257
 E value 4.0e-22
 Match length 74
 % identity 76
 NCBI Description ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi_67880_pir_PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase

07E84016-101000

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Seq. No.      398090
Seq. ID      LIB3431-010-P1-N1-A3
Method       BLASTN
NCBI GI      g218209
BLAST score   124
E value      3.0e-63
Match length  248
% identity    98
NCBI Description  Oryza sativa mRNA for the small subunit of
ribulose-1,5-bisphosphate carboxylase, complete cds, clone
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0969016-70100

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Seq. No.      398095
Seq. ID      LIB3431-010-P1-N1-B4
Method      BLASTN
```


(gamma subunit) [Nicotiana tabacum]

Seq. No. 398111
 Seq. ID LIB3431-010-P1-N1-E5
 Method BLASTN
 NCBI GI g11957
 BLAST score 133
 E value 1.0e-68
 Match length 169
 % identity 47
 NCBI Description Rice complete chloroplast genome

Seq. No. 398112
 Seq. ID LIB3431-010-P1-N1-E9
 Method BLASTN
 NCBI GI g20181
 BLAST score 160
 E value 1.0e-84
 Match length 179
 % identity 98
 NCBI Description Rice cab2R gene for light harvesting chlorophyll
 a/b-binding protein

Seq. No. 398113
 Seq. ID LIB3431-010-P1-N1-F1
 Method BLASTN
 NCBI GI g218207
 BLAST score 217
 E value 1.0e-119
 Match length 221
 % identity 100
 NCBI Description Oryza sativa mRNA for the small subunit of
 ribulose-1,5-bisphosphate carboxylase, complete cds, clone
 pOSSS1139

Seq. No. 398114
 Seq. ID LIB3431-010-P1-N1-F11
 Method BLASTN
 NCBI GI g6016845
 BLAST score 204
 E value 1.0e-111
 Match length 240
 % identity 96
 NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No. 398115
 Seq. ID LIB3431-010-P1-N1-F12
 Method BLASTX
 NCBI GI g266893
 BLAST score 637
 E value 8.0e-67
 Match length 123
 % identity 98
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
 CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
 >gi_322416_pir_S28172 ribulose-bisphosphate carboxylase
 activase - cucumber >gi_18284_emb_CAA47906_ (X67674)

rubisco activase [Cucumis sativus]

Seq. No. 398116
 Seq. ID LIB3431-010-P1-N1-F3
 Method BLASTN
 NCBI GI g288058
 BLAST score 53
 E value 6.0e-21
 Match length 73
 % identity 93
 NCBI Description Z.mays S13 mRNA for cytoplasmic ribosomal protein S13

Seq. No. 398117
 Seq. ID LIB3431-010-P1-N1-G1
 Method BLASTN
 NCBI GI g2661765
 BLAST score 50
 E value 4.0e-19
 Match length 82
 % identity 90
 NCBI Description Zea mays mRNA for putative porphobilinogen deaminase

Seq. No. 398118
 Seq. ID LIB3431-010-P1-N1-G11
 Method BLASTN
 NCBI GI g218154
 BLAST score 80
 E value 6.0e-37
 Match length 145
 % identity 100
 NCBI Description Oryza sativa gene for cytoplasmic aldolase, complete cds, clone:Aldp

Seq. No. 398119
 Seq. ID LIB3431-010-P1-N1-G12
 Method BLASTN
 NCBI GI g2662340
 BLAST score 269
 E value 1.0e-150
 Match length 316
 % identity 96
 NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds

Seq. No. 398120
 Seq. ID LIB3431-010-P1-N1-G2
 Method BLASTX
 NCBI GI g125606
 BLAST score 250
 E value 2.0e-21
 Match length 59
 % identity 86
 NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir__S12248
 pyruvate kinase (EC 2.7.1.40) - potato
 >gi_22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum
 tuberosum]

Seq. No. 398121

Seq. ID LIB3431-010-P1-N1-G5
 Method BLASTX
 NCBI GI g548603
 BLAST score 225
 E value 2.0e-18
 Match length 56
 % identity 80
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
 (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
 >gi_478404_pir_JQ2247 photosystem I chain D precursor -
 barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 398122
 Seq. ID LIB3431-010-P1-N1-G7
 Method BLASTX
 NCBI GI g1835731
 BLAST score 297
 E value 5.0e-27
 Match length 67
 % identity 85
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 398123
 Seq. ID LIB3431-010-P1-N1-G8
 Method BLASTX
 NCBI GI g132096
 BLAST score 154
 E value 3.0e-10
 Match length 29
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN A PRECURSOR
 (RUBISCO SMALL SUBUNIT A) >gi_68095_pir_RKRZS6
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS2106) - rice >gi_218210_dbj_BAA00539_
 (D00644) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa]

Seq. No. 398124
 Seq. ID LIB3431-010-P1-N1-G9
 Method BLASTX
 NCBI GI g3126854
 BLAST score 300
 E value 2.0e-27
 Match length 57
 % identity 100
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 398125
 Seq. ID LIB3431-010-P1-N1-H1
 Method BLASTX
 NCBI GI g606817
 BLAST score 154
 E value 4.0e-10
 Match length 28
 % identity 100
 NCBI Description (U08404) carbonic anhydrase [Oryza sativa]
 >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic

050840J 03 101000

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Seq. No.      398127
Seq. ID      LIB3431-010-P1-N1-H4
Method       BLASTX
NCBI GI      g548605
BLAST score   239
E value      1.0e-28
Match length  80
% identity    89
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                >gi_539055_pir_A48527 photosystem I protein psaK precursor
                - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                [Hordeum vulgare]
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Seq. No.	398128
Seq. ID	LIB3431-010-P1-N1-H6
Method	BLASTN
NCBI GI	g1136121
BLAST score	321
E value	0.0e+00
Match length	324
% identity	100
NCBI Description	O.sativa mRNA for alpha-tubulin (clone OSTA-136)

Seq. No.	398129
Seq. ID	LIB3431-010-P1-N1-H7
Method	BLASTN
NCBI GI	g2737972
BLAST score	38
E value	6.0e-12
Match length	74
% identity	88
NCBI Description	Zea mays protein kinase ZmMEK1 mRNA, complete cds

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Seq. No.          398130
Seq. ID           LIB3431-011-P1-K1-A10
Method            BLASTX
NCBI GI           g1742187
BLAST score       170
E value           6.0e-12
Match length      121
% identity        35
NCBI Description   (D90771) ORF ID:o260#14; similar to [SwissProt Accession
                  Number P11666] [Escherichia coli] >gi_1742198_dbj_BAA14933_
                  (D90772) ORF ID:o260#14; similar to [SwissProt Accession
```


% identity 83
 NCBI Description (AC007018) putative ribosomal protein S17 [Arabidopsis thaliana]

Seq. No. 398136
 Seq. ID LIB3431-011-P1-K1-B12
 Method BLASTX
 NCBI GI g131225
 BLAST score 301
 E value 3.0e-27
 Match length 93
 % identity 61
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 398137
 Seq. ID LIB3431-011-P1-K1-B2
 Method BLASTX
 NCBI GI g1621477
 BLAST score 378
 E value 2.0e-36
 Match length 81
 % identity 85
 NCBI Description (D85868) reverse transcriptase [Oryza sativa]

Seq. No. 398138
 Seq. ID LIB3431-011-P1-K1-B4
 Method BLASTX
 NCBI GI g5880709
 BLAST score 205
 E value 3.0e-16
 Match length 43
 % identity 100
 NCBI Description (AF137379) CF0 subunit III of ATP synthase [Nephroselmis olivacea]

Seq. No. 398139
 Seq. ID LIB3431-011-P1-K1-B5
 Method BLASTX
 NCBI GI g3850566
 BLAST score 263
 E value 7.0e-23
 Match length 134
 % identity 43
 NCBI Description (AC005278) F15K9.3 [Arabidopsis thaliana]

Seq. No. 398140
 Seq. ID LIB3431-011-P1-K1-B6
 Method BLASTN
 NCBI GI g218207
 BLAST score 294
 E value 1.0e-164
 Match length 298
 % identity 100
 NCBI Description Oryza sativa mRNA for the small subunit of

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 398146
 Seq. ID LIB3431-011-P1-K1-C7
 Method BLASTX
 NCBI GI g133999
 BLAST score 493
 E value 7.0e-50
 Match length 100
 % identity 100
 NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S7 >gi_70904_pir_R3RZ7 ribosomal protein S7 - rice chloroplast >gi_12037_emb_CAA33942_(X15901) ribosomal protein S7 [Oryza sativa] >gi_12065_emb_CAA33919_(X15901) ribosomal protein S7 [Oryza sativa] >gi_226657_prf_1603356CH ribosomal protein S7 [Oryza sativa]

Seq. No. 398147
 Seq. ID LIB3431-011-P1-K1-C8
 Method BLASTX
 NCBI GI g2625084
 BLAST score 550
 E value 1.0e-56
 Match length 129
 % identity 85
 NCBI Description (AF030382) ADP-glucose pyrophosphorylase small subunit [Cucumis melo var. markuwa Markino]

Seq. No. 398148
 Seq. ID LIB3431-011-P1-K1-C9
 Method BLASTN
 NCBI GI g4574134
 BLAST score 123
 E value 6.0e-63
 Match length 146
 % identity 97
 NCBI Description Oryza sativa cysteine synthase (rcs1) mRNA, complete cds

Seq. No. 398149
 Seq. ID LIB3431-011-P1-K1-D1
 Method BLASTN
 NCBI GI g6015437
 BLAST score 36
 E value 1.0e-10
 Match length 49
 % identity 65
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 398150
 Seq. ID LIB3431-011-P1-K1-D11
 Method BLASTX

% identity 96
 NCBI Description O.sativa light-induced mRNA

Seq. No. 398161
 Seq. ID LIB3431-011-P1-K1-E4
 Method BLASTX
 NCBI GI g3047109
 BLAST score 206
 E value 3.0e-16
 Match length 90
 % identity 49
 NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 398162
 Seq. ID LIB3431-011-P1-K1-E6
 Method BLASTX
 NCBI GI g3941480
 BLAST score 288
 E value 1.0e-25
 Match length 129
 % identity 49
 NCBI Description (AF062894) putative transcription factor [Arabidopsis thaliana]

Seq. No. 398163
 Seq. ID LIB3431-011-P1-K1-E8
 Method BLASTX
 NCBI GI g5679336
 BLAST score 253
 E value 9.0e-22
 Match length 94
 % identity 49
 NCBI Description (AF171223) putative zinc finger protein [Oryza sativa]

Seq. No. 398164
 Seq. ID LIB3431-011-P1-K1-F10
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 4.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 398165
 Seq. ID LIB3431-011-P1-K1-F4
 Method BLASTN
 NCBI GI g3377792
 BLAST score 67
 E value 7.0e-30
 Match length 83
 % identity 95
 NCBI Description Oryza sativa ribulose-1,5-bisphosphate carboxylase/oxygenase activase (rca) mRNA, complete cds

Seq. No. 398181
 Seq. ID LIB3431-011-P1-K1-H4
 Method BLASTX
 NCBI GI g4886307
 BLAST score 704
 E value 1.0e-74
 Match length 135
 % identity 97
 NCBI Description (AJ242588) 1-deoxy-d-xylulose-5-phosphate reductoisomerase
 [Arabidopsis thaliana]

Seq. No. 398182
 Seq. ID LIB3431-011-P1-K1-H5
 Method BLASTX
 NCBI GI g3345477
 BLAST score 314
 E value 6.0e-29
 Match length 111
 % identity 58
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 398183
 Seq. ID LIB3431-011-P1-K1-H7
 Method BLASTX
 NCBI GI g733458
 BLAST score 484
 E value 9.0e-49
 Match length 109
 % identity 84
 NCBI Description (U23190) chlorophyll a/b-binding apoprotein CP24 precursor
 [Zea mays]

Seq. No. 398184
 Seq. ID LIB3431-011-P1-K1-H9
 Method BLASTX
 NCBI GI g320618
 BLAST score 386
 E value 1.0e-40
 Match length 116
 % identity 78
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 398185
 Seq. ID LIB3431-011-P1-N1-A1
 Method BLASTX
 NCBI GI g542157
 BLAST score 528
 E value 5.0e-54
 Match length 124
 % identity 85
 NCBI Description ribosomal 5S RNA-binding protein - Rice

Seq. No. 398186

000001-01000

Seq. ID LIB3431-011-P1-N1-B2
 Method BLASTX
 NCBI GI g3377848
 BLAST score 198
 E value 3.0e-15
 Match length 95
 % identity 38
 NCBI Description (AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]

Seq. No. 398192
 Seq. ID LIB3431-011-P1-N1-B3
 Method BLASTX
 NCBI GI g6093830
 BLAST score 211
 E value 1.0e-16
 Match length 94
 % identity 34
 NCBI Description PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME) [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II PROTEIN PSBY-2] >gi_3337435 (AF060198) PsbY precursor; putative photosytem II peptide [Spinacia oleracea]

Seq. No. 398193
 Seq. ID LIB3431-011-P1-N1-B4
 Method BLASTN
 NCBI GI g11957
 BLAST score 341
 E value 0.0e+00
 Match length 362
 % identity 98
 NCBI Description Rice complete chloroplast genome

Seq. No. 398194
 Seq. ID LIB3431-011-P1-N1-B5
 Method BLASTX
 NCBI GI g3924605
 BLAST score 251
 E value 2.0e-21
 Match length 59
 % identity 71
 NCBI Description (AF069442) putative inhibitor of apoptosis [Arabidopsis thaliana]

Seq. No. 398195
 Seq. ID LIB3431-011-P1-N1-B6
 Method BLASTN
 NCBI GI g218207
 BLAST score 298
 E value 1.0e-167
 Match length 298
 % identity 100
 NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone poSSS1139

Seq. No. 398196

Seq. ID LIB3431-011-P1-N1-B9
 Method BLASTX
 NCBI GI g421855
 BLAST score 151
 E value 1.0e-09
 Match length 79
 % identity 44
 NCBI Description alanine--tRNA ligase (EC 6.1.1.7) - Arabidopsis thaliana (fragment)

Seq. No. 398197
 Seq. ID LIB3431-011-P1-N1-C10
 Method BLASTX
 NCBI GI g3929924
 BLAST score 163
 E value 3.0e-11
 Match length 36
 % identity 89
 NCBI Description (AB020502) catalase [Oryza sativa]

Seq. No. 398198
 Seq. ID LIB3431-011-P1-N1-C3
 Method BLASTX
 NCBI GI g1504052
 BLAST score 270
 E value 1.0e-23
 Match length 52
 % identity 100
 NCBI Description (D87042) Calcium-dependent protein kinase [Zea mays]

Seq. No. 398199
 Seq. ID LIB3431-011-P1-N1-C5
 Method BLASTX
 NCBI GI g289920
 BLAST score 217
 E value 1.0e-17
 Match length 42
 % identity 98
 NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No. 398200
 Seq. ID LIB3431-011-P1-N1-C6
 Method BLASTX
 NCBI GI g132105
 BLAST score 289
 E value 8.0e-26
 Match length 73
 % identity 78
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate

0564016 701000

Seq. No.	398202
Seq. ID	LIB3431-011-P1-N1-C9
Method	BLASTN
NCBI GI	g4574134
BLAST score	147
E value	3.0e-77
Match length	147
% identity	100
NCBI Description	Oryza sativa cysteine synthase (rcs1) mRNA, complete cds

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Seq. No.      398204
Seq. ID      LIB3431-011-P1-N1-D3
Method       BLASTX
NCBI GI      g3885892
BLAST score   426
E value      6.0e-42
Match length  83
% identity    98
NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
```

Seq. No.	398206
Seq. ID	LIB3431-011-P1-N1-D9
Method	BLASTN

NCBI GI g218209
 BLAST score 149
 E value 4.0e-78
 Match length 299
 % identity 97
 NCBI Description Oryza sativa mRNA for the small subunit of
 ribulose-1,5-bisphosphate carboxylase, complete cds, clone
 pOSSS2106

Seq. No. 398207
 Seq. ID LIB3431-011-P1-N1-E12
 Method BLASTX
 NCBI GI g115802
 BLAST score 217
 E value 1.0e-17
 Match length 40
 % identity 100
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I
 CAB-36) (LHCP) >gi_100311_pir_S21827 chlorophyll
 a/b-binding protein (cab-36) - common tobacco
 >gi_19827_emb_CAA41188_ (X58230) chlorophyll a/b binding
 protein [Nicotiana tabacum]

Seq. No. 398208
 Seq. ID LIB3431-011-P1-N1-E3
 Method BLASTX
 NCBI GI g417260
 BLAST score 326
 E value 3.0e-30
 Match length 81
 % identity 77
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

Seq. No. 398209
 Seq. ID LIB3431-011-P1-N1-E5
 Method BLASTX
 NCBI GI g517500
 BLAST score 234
 E value 1.0e-19
 Match length 79
 % identity 62
 NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa
 protein [Zea mays] >gi_444338_prf_1906386A photosystem II
 OE17 protein [Pisum sativum]

Seq. No. 398210
 Seq. ID LIB3431-011-P1-N1-E9
 Method BLASTX
 NCBI GI g3212877
 BLAST score 180
 E value 3.0e-13
 Match length 40
 % identity 85
 NCBI Description (AC004005) Lea-like protein [Arabidopsis thaliana]

E value	3.0e-09
Match length	30
% identity	87
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I CAB-36) (LHCP) >gi_100311_pir_S21827 chlorophyll a/b-binding protein (cab-36) - common tobacco >gi_19827_emb_CAA41188_ (X58230) chlorophyll a/b binding protein [Nicotiana tabacum]
Seq. No.	398216
Seq. ID	LIB3431-011-P1-N1-F8
Method	BLASTX
NCBI GI	g3036949
BLAST score	264
E value	4.0e-23
Match length	50
% identity	100
NCBI Description	(AB012638) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]
Seq. No.	398217
Seq. ID	LIB3431-011-P1-N1-F9
Method	BLASTX
NCBI GI	g1076678
BLAST score	243
E value	1.0e-20
Match length	48
% identity	100
NCBI Description	ubiquitin / ribosomal protein S27a - potato (fragment)
Seq. No.	398218
Seq. ID	LIB3431-011-P1-N1-G1
Method	BLASTX
NCBI GI	g131176
BLAST score	304
E value	1.0e-27
Match length	59
% identity	98
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E) >gi_72683_pir_FLBH4 photosystem I chain IV precursor - barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf_1413233A 10.8kD photosystem I protein [Hordeum vulgare var. distichum]
Seq. No.	398219
Seq. ID	LIB3431-011-P1-N1-G12
Method	BLASTN
NCBI GI	g3789951
BLAST score	191
E value	1.0e-103
Match length	414
% identity	99
NCBI Description	Oryza sativa chlorophyll a/b-binding protein precursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 398220
 Seq. ID LIB3431-011-P1-N1-G2
 Method BLASTX
 NCBI GI g6006283
 BLAST score 151
 E value 8.0e-10
 Match length 41
 % identity 73
 NCBI Description (AB015861) photosystem I subunit PSI-L [Arabidopsis thaliana]

Seq. No. 398221
 Seq. ID LIB3431-011-P1-N1-G4
 Method BLASTX
 NCBI GI g548605
 BLAST score 402
 E value 9.0e-40
 Match length 105
 % identity 87
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir_A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No. 398222
 Seq. ID LIB3431-011-P1-N1-G5
 Method BLASTX
 NCBI GI g3738261
 BLAST score 416
 E value 9.0e-41
 Match length 91
 % identity 92
 NCBI Description (AB018412) chloroplast phosphoglycerate kinase [Populus nigra]

Seq. No. 398223
 Seq. ID LIB3431-011-P1-N1-G9
 Method BLASTX
 NCBI GI g485512
 BLAST score 326
 E value 3.0e-30
 Match length 70
 % identity 87
 NCBI Description salt-associated protein csaA - sweet orange

Seq. No. 398224
 Seq. ID LIB3431-011-P1-N1-H10
 Method BLASTX
 NCBI GI g2754849
 BLAST score 186
 E value 7.0e-14
 Match length 43
 % identity 84
 NCBI Description (AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

Seq. ID LIB3431-012-P1-K1-B5
 Method BLASTN
 NCBI GI g3789951
 BLAST score 62
 E value 3.0e-26
 Match length 121
 % identity 88
 NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor
 (Cab27) mRNA, nuclear gene encoding chloroplast protein,
 complete cds

Seq. No. 398241
 Seq. ID LIB3431-012-P1-K1-B6
 Method BLASTX
 NCBI GI g3075488
 BLAST score 211
 E value 3.0e-17
 Match length 59
 % identity 69
 NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 398242
 Seq. ID LIB3431-012-P1-K1-B8
 Method BLASTX
 NCBI GI g548603
 BLAST score 380
 E value 1.0e-36
 Match length 120
 % identity 68
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
 (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
 >gi_478404_pir_JQ2247 photosystem I chain D precursor -
 barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 398243
 Seq. ID LIB3431-012-P1-K1-B9
 Method BLASTX
 NCBI GI g131225
 BLAST score 378
 E value 1.0e-36
 Match length 85
 % identity 88
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
 V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein
 precursor - barley >gi_167087 (M61146) photosystem I
 hydrophobic protein [Hordeum vulgare]

Seq. No. 398244
 Seq. ID LIB3431-012-P1-K1-C1
 Method BLASTX
 NCBI GI g1707018
 BLAST score 460
 E value 7.0e-46
 Match length 104
 % identity 86
 NCBI Description (U78721) CutA isolog [Arabidopsis thaliana]

Seq. No. 398245
 Seq. ID LIB3431-012-P1-K1-C11
 Method BLASTX
 NCBI GI g2244867
 BLAST score 298
 E value 6.0e-27
 Match length 137
 % identity 44
 NCBI Description (Z97337) hydroxynitrile lyase like protein [Arabidopsis thaliana]

Seq. No. 398246
 Seq. ID LIB3431-012-P1-K1-C2
 Method BLASTX
 NCBI GI g2072555
 BLAST score 208
 E value 3.0e-16
 Match length 62
 % identity 63
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 398247
 Seq. ID LIB3431-012-P1-K1-C3
 Method BLASTX
 NCBI GI g4079798
 BLAST score 223
 E value 2.0e-18
 Match length 46
 % identity 96
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 398248
 Seq. ID LIB3431-012-P1-K1-C4
 Method BLASTX
 NCBI GI g2407281
 BLAST score 304
 E value 1.0e-27
 Match length 87
 % identity 68
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 398249
 Seq. ID LIB3431-012-P1-K1-C5
 Method BLASTX
 NCBI GI g1353352
 BLAST score 423
 E value 2.0e-41
 Match length 116
 % identity 72
 NCBI Description (U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No. 398250

09684016 "101000

Seq. ID	LIB3431-012-P1-K1-C7
Method	BLASTN
NCBI GI	g1944204
BLAST score	451
E value	0.0e+00
Match length	466
% identity	99
NCBI Description	Oryza sativa mRNA for RicMT, complete cds
Seq. No.	398251
Seq. ID	LIB3431-012-P1-K1-C8
Method	BLASTX
NCBI GI	g4585142
BLAST score	388
E value	2.0e-37
Match length	101
% identity	71
NCBI Description	(AF088276) NADPH oxidase; gp91; phox homolog [Lycopersicon esculentum]
Seq. No.	398252
Seq. ID	LIB3431-012-P1-K1-C9
Method	BLASTX
NCBI GI	g170131
BLAST score	176
E value	1.0e-12
Match length	48
% identity	62
NCBI Description	(M55322) ribosomal protein 30S subunit [Spinacia oleracea]
Seq. No.	398253
Seq. ID	LIB3431-012-P1-K1-D1
Method	BLASTX
NCBI GI	g5091623
BLAST score	521
E value	5.0e-53
Match length	125
% identity	82
NCBI Description	(AC007454) Similar to gb_U93048 somatic embryogenesis receptor-like kinase from Daucus carota, contains 4 PF_00560 Leucine Rich Repeat domains and a PF_00069 Eukaryotic protein kinase domain. [Arabidopsis thaliana]
Seq. No.	398254
Seq. ID	LIB3431-012-P1-K1-D10
Method	BLASTX
NCBI GI	g4510363
BLAST score	511
E value	6.0e-52
Match length	123
% identity	80
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]
Seq. No.	398255
Seq. ID	LIB3431-012-P1-K1-D12
Method	BLASTX

NCBI GI g6056373
 BLAST score 218
 E value 1.0e-19
 Match length 102
 % identity 59
 NCBI Description (AC009894) elongation factor EF-2 [Arabidopsis thaliana]

Seq. No. 398256
 Seq. ID LIB3431-012-P1-K1-D2
 Method BLASTX
 NCBI GI g733454
 BLAST score 575
 E value 2.0e-59
 Match length 133
 % identity 82
 NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No. 398257
 Seq. ID LIB3431-012-P1-K1-D4
 Method BLASTN
 NCBI GI g20239
 BLAST score 119
 E value 4.0e-60
 Match length 135
 % identity 97
 NCBI Description O.sativa (rice) shoot-specific GOS5 gene for a putative chloroplast transit peptide

Seq. No. 398258
 Seq. ID LIB3431-012-P1-K1-D6
 Method BLASTX
 NCBI GI g1055130
 BLAST score 220
 E value 8.0e-18
 Match length 131
 % identity 44
 NCBI Description (U39998) coded for by C. elegans cDNA yk92b11.3; coded for by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA yk78c2.5; coded for by C. elegans cDNA cm9a8; coded for by C. elegans cDNA yk66h8.3; coded for by C. elegans cDNA yk78c2.3

Seq. No. 398259
 Seq. ID LIB3431-012-P1-K1-D8
 Method BLASTX
 NCBI GI g3522929
 BLAST score 589
 E value 5.0e-61
 Match length 126
 % identity 87
 NCBI Description (AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi_3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No. 398260
 Seq. ID LIB3431-012-P1-K1-D9

Method BLASTX
 NCBI GI g115787
 BLAST score 365
 E value 4.0e-35
 Match length 94
 % identity 81
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 398261
 Seq. ID LIB3431-012-P1-K1-E10
 Method BLASTX
 NCBI GI g115794
 BLAST score 787
 E value 3.0e-84
 Match length 156
 % identity 93
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE III CAB-13) >gi_72748_pir_CDT033 chlorophyll a/b-binding protein type III precursor (cab-13) - tomato >gi_19277_emb_CAA42818_ (X60275) LHCII type III [Lycopersicon esculentum]

Seq. No. 398262
 Seq. ID LIB3431-012-P1-K1-E11
 Method BLASTX
 NCBI GI g4239891
 BLAST score 617
 E value 3.0e-67
 Match length 151
 % identity 87
 NCBI Description (AB016804) NADP-malic enzyme [Aloe arborescens]

Seq. No. 398263
 Seq. ID LIB3431-012-P1-K1-E12
 Method BLASTX
 NCBI GI g115787
 BLAST score 352
 E value 2.0e-33
 Match length 90
 % identity 80
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 398264
 Seq. ID LIB3431-012-P1-K1-E4
 Method BLASTX
 NCBI GI g4531444
 BLAST score 472
 E value 3.0e-47
 Match length 148

% identity 83
 NCBI Description (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
 [Zea mays]

Seq. No. 398270
 Seq. ID LIB3431-012-P1-K1-F12
 Method BLASTX
 NCBI GI g1835731
 BLAST score 455
 E value 2.0e-45
 Match length 93
 % identity 95
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 398271
 Seq. ID LIB3431-012-P1-K1-F9
 Method BLASTN
 NCBI GI g3885891
 BLAST score 144
 E value 3.0e-75
 Match length 197
 % identity 98
 NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F)
 mRNA, complete cds

Seq. No. 398272
 Seq. ID LIB3431-012-P1-K1-G1
 Method BLASTN
 NCBI GI g3885891
 BLAST score 105
 E value 3.0e-52
 Match length 125
 % identity 96
 NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F)
 mRNA, complete cds

Seq. No. 398273
 Seq. ID LIB3431-012-P1-K1-G10
 Method BLASTX
 NCBI GI g2754849
 BLAST score 278
 E value 4.0e-25
 Match length 64
 % identity 84
 NCBI Description (AF039000) putative serine-glyoxylate aminotransferase
 [Fritillaria agrestis]

Seq. No. 398274
 Seq. ID LIB3431-012-P1-K1-G12
 Method BLASTX
 NCBI GI g1632822
 BLAST score 461
 E value 3.0e-46
 Match length 92
 % identity 97
 NCBI Description (Y08962) transmembrane protein [Oryza sativa] >gi_1667594
 (U77297) transmembrane protein [Oryza sativa]

Seq. No. 398275
 Seq. ID LIB3431-012-P1-K1-G2
 Method BLASTX
 NCBI GI g115525
 BLAST score 162
 E value 8.0e-19
 Match length 78
 % identity 67
 NCBI Description CALMODULIN >gi_71685_pir_MCSP calmodulin - spinach

Seq. No. 398276
 Seq. ID LIB3431-012-P1-K1-G3
 Method BLASTX
 NCBI GI g1709846
 BLAST score 226
 E value 2.0e-18
 Match length 133
 % identity 38
 NCBI Description PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_706853 (U04336)
 22 kDa component of photosystem II [Lycopersicon
 esculentum]

Seq. No. 398277
 Seq. ID LIB3431-012-P1-K1-G5
 Method BLASTX
 NCBI GI g2407281
 BLAST score 626
 E value 2.0e-65
 Match length 128
 % identity 91
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
 subunit [Oryza sativa]

Seq. No. 398278
 Seq. ID LIB3431-012-P1-K1-G6
 Method BLASTX
 NCBI GI g1353352
 BLAST score 342
 E value 5.0e-32
 Match length 104
 % identity 63
 NCBI Description (U31975) alanine aminotransferase [Chlamydomonas
 reinhardtii]

Seq. No. 398279
 Seq. ID LIB3431-012-P1-K1-G7
 Method BLASTX
 NCBI GI g122106
 BLAST score 389
 E value 1.0e-37
 Match length 79
 % identity 99
 NCBI Description HISTONE H4 >gi_70771_pir_HSZM4 histone H4 - maize
 >gi_81642_pir_S06904 histone H4 - Arabidopsis thaliana
 >gi_2119028_pir_S60475 histone H4 - garden pea
 >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum

aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays] >gi_168501 (M13370) histone H4 [Zea mays] >gi_168503 (M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata] >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi_6009915_dbj_BAA85120.1_ (AB018245) histone H4-like protein [Solanum melongena] >gi_225838_prf_1314298A histone H4 [Arabidopsis thaliana]

Seq. No. 398280
Seq. ID LIB3431-012-P1-K1-G9
Method BLASTX
NCBI GI g3075382
BLAST score 212
E value 7.0e-17
Match length 110
% identity 50
NCBI Description (AC002505) putative peroxisome assembly protein PER8 [Arabidopsis thaliana] >gi_3075384 (AC004484) putative peroxisome assembly protein PER8 [Arabidopsis thaliana]

Seq. No. 398281
Seq. ID LIB3431-012-P1-K1-H1
Method BLASTX
NCBI GI g3355477
BLAST score 441
E value 1.0e-43
Match length 105
% identity 44
NCBI Description (AC004218) putative P-glycoprotein, pgp1 [Arabidopsis thaliana]

Seq. No. 398282
Seq. ID LIB3431-012-P1-K1-H10
Method BLASTN
NCBI GI g6015437
BLAST score 36
E value 1.0e-11
Match length 36
% identity 100
NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 398283
Seq. ID LIB3431-012-P1-K1-H2
Method BLASTX
NCBI GI g4102703
BLAST score 468
E value 1.0e-52
Match length 140
% identity 79
NCBI Description (AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis thaliana]

Seq. No. 398284
 Seq. ID LIB3431-012-P1-K1-H3
 Method BLASTX
 NCBI GI g2653558
 BLAST score 776
 E value 6.0e-83
 Match length 159
 % identity 91
 NCBI Description (D50679) ferredoxin-sulfite reductase precursor [Zea mays]

Seq. No. 398285
 Seq. ID LIB3431-012-P1-K1-H5
 Method BLASTX
 NCBI GI g2982453
 BLAST score 295
 E value 4.0e-27
 Match length 63
 % identity 94
 NCBI Description (AL022223) fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana]

Seq. No. 398286
 Seq. ID LIB3431-012-P1-K1-H7
 Method BLASTX
 NCBI GI g115787
 BLAST score 280
 E value 3.0e-25
 Match length 77
 % identity 77
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 398287
 Seq. ID LIB3431-012-P1-K1-H8
 Method BLASTX
 NCBI GI g3345477
 BLAST score 429
 E value 3.0e-42
 Match length 128
 % identity 68
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 398288
 Seq. ID LIB3431-012-P1-K1-H9
 Method BLASTN
 NCBI GI g4887617
 BLAST score 131
 E value 2.0e-67
 Match length 142
 % identity 98
 NCBI Description Oryza sativa HOS59 mRNA, partial cds

Seq. No. 398289
 Seq. ID LIB3431-013-P1-K1-A10

Method BLASTX
 NCBI GI g2673914
 BLAST score 325
 E value 8.0e-42
 Match length 139
 % identity 62
 NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No. 398290
 Seq. ID LIB3431-013-P1-K1-A12
 Method BLASTX
 NCBI GI g2660669
 BLAST score 311
 E value 2.0e-28
 Match length 131
 % identity 47
 NCBI Description (AC002342) human Mi-2 autoantigen-like protein [Arabidopsis thaliana]

Seq. No. 398291
 Seq. ID LIB3431-013-P1-K1-A4
 Method BLASTX
 NCBI GI g132105
 BLAST score 417
 E value 5.0e-43
 Match length 130
 % identity 76
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 398292
 Seq. ID LIB3431-013-P1-K1-A5
 Method BLASTX
 NCBI GI g4206195
 BLAST score 213
 E value 5.0e-17
 Match length 54
 % identity 67
 NCBI Description (AF071527) hypothetical protein [Arabidopsis thaliana] >gi_4262169_gb_AAD14469_ (AC005275) hypothetical protein [Arabidopsis thaliana]

Seq. No. 398293
 Seq. ID LIB3431-013-P1-K1-A6
 Method BLASTN
 NCBI GI g6015437
 BLAST score 36
 E value 1.0e-10
 Match length 36
 % identity 100

Seq. No. 398299
 Seq. ID LIB3431-013-P1-K1-B12
 Method BLASTX
 NCBI GI g1169798
 BLAST score 336
 E value 2.0e-31
 Match length 85
 % identity 79
 NCBI Description GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC B (GPI-B)
 (PHOSPHOGLUCOSE ISOMERASE B) (PGI-B) (PHOSPHOHEXOSE
 ISOMERASE B) (PHI-B) >gi_639686_dbj_BAA08149_ (D45218)
 phosphoglucose isomerase (Pgi-b) [Oryza sativa]

Seq. No. 398300
 Seq. ID LIB3431-013-P1-K1-B2
 Method BLASTX
 NCBI GI g132105
 BLAST score 501
 E value 1.0e-52
 Match length 134
 % identity 81
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor. (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 398301
 Seq. ID LIB3431-013-P1-K1-B3
 Method BLASTN
 NCBI GI g6002093
 BLAST score 52
 E value 9.0e-21
 Match length 63
 % identity 97
 NCBI Description Zizania latifolia chloroplast rps4 gene for ribosomal
 protein S4

Seq. No. 398302
 Seq. ID LIB3431-013-P1-K1-B4
 Method BLASTX
 NCBI GI g488573
 BLAST score 600
 E value 2.0e-62
 Match length 122
 % identity 98
 NCBI Description (U09463) histone H3.2 [Medicago sativa]

Seq. No. 398303
 Seq. ID LIB3431-013-P1-K1-B7
 Method BLASTX
 NCBI GI g3757521

Seq. No. 398309
 Seq. ID LIB3431-013-P1-K1-C5
 Method BLASTX
 NCBI GI g131225
 BLAST score 511
 E value 6.0e-52
 Match length 111
 % identity 88
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 398310
 Seq. ID LIB3431-013-P1-K1-C6
 Method BLASTX
 NCBI GI g461899
 BLAST score 184
 E value 1.0e-13
 Match length 116
 % identity 40
 NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST PRECURSOR (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_1076368_pir_B53422 peptidylprolyl isomerase (EC 5.2.1.8) ROC4 - Arabidopsis thaliana >gi_405131 (L14845) cyclophilin [Arabidopsis thaliana] >gi_1322278 (U42724) cyclophilin [Arabidopsis thaliana]

Seq. No. 398311
 Seq. ID LIB3431-013-P1-K1-C7
 Method BLASTX
 NCBI GI g3914466
 BLAST score 199
 E value 2.0e-15
 Match length 36
 % identity 97
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN subunit precursor [Zea mays]

Seq. No. 398312
 Seq. ID LIB3431-013-P1-K1-C9
 Method BLASTX
 NCBI GI g4512653
 BLAST score 225
 E value 2.0e-18
 Match length 51
 % identity 82
 NCBI Description (AC007048) unknown protein [Arabidopsis thaliana]

Seq. No. 398313
 Seq. ID LIB3431-013-P1-K1-D10
 Method BLASTX
 NCBI GI g121343
 BLAST score 729
 E value 2.0e-77

Match length 138
 % identity 99
 NCBI Description GLUTAMINE SYNTHETASE SHOOT ISOZYME, CHLOROPLAST PRECURSOR
 (GLUTAMATE--AMMONIA LIGASE) (CLONE LAMBDA-GS31)
 >gi_68598_pir_AJRZQD glutamate--ammonia ligase (EC
 6.3.1.2) delta precursor, chloroplast - rice
 >gi_20370_emb_CAA32462_ (X14246) precursor chloroplastic
 glutamine synthetase (AA -46 to 382) [Oryza sativa]

Seq. No. 398314
 Seq. ID LIB3431-013-P1-K1-D11
 Method BLASTX
 NCBI GI g3789952
 BLAST score 566
 E value 1.0e-58
 Match length 127
 % identity 94
 NCBI Description (AF094775) chlorophyll a/b-binding protein precursor [Oryza
 sativa]

Seq. No. 398315
 Seq. ID LIB3431-013-P1-K1-D12
 Method BLASTX
 NCBI GI g3913240
 BLAST score 401
 E value 5.0e-39
 Match length 94
 % identity 90
 NCBI Description MAGNESIUM-CHELATASE SUBUNIT CHLD PRECURSOR
 (MG-PROTOPORPHYRIN IX CHELATASE) (MG-CHELATASE SUBUNIT D)
 >gi_2239151_emb_CAA71128_ (Y10022) CHLD magnesium chelatase
 subunit [Nicotiana tabacum]

Seq. No. 398316
 Seq. ID LIB3431-013-P1-K1-D2
 Method BLASTX
 NCBI GI g132105
 BLAST score 178
 E value 2.0e-13
 Match length 55
 % identity 67
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 398317
 Seq. ID LIB3431-013-P1-K1-D3
 Method BLASTX
 NCBI GI g82080
 BLAST score 383
 E value 6.0e-37

Match length 107
 % identity 67
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
 >gi_226872_prf_1609235A chlorophyll a/b binding protein
 [Lycopersicon esculentum]

Seq. No. 398318
 Seq. ID LIB3431-013-P1-K1-D5
 Method BLASTX
 NCBI GI g417260
 BLAST score 421
 E value 2.0e-41
 Match length 128
 % identity 66
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

Seq. No. 398319
 Seq. ID LIB3431-013-P1-K1-D9
 Method BLASTX
 NCBI GI g100615
 BLAST score 732
 E value 8.0e-78
 Match length 143
 % identity 96
 NCBI Description ribulose-bisphosphate carboxylase activase A short form
 precursor - barley >gi_167091 (M55447) ribulose
 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No. 398320
 Seq. ID LIB3431-013-P1-K1-E1
 Method BLASTX
 NCBI GI g671740
 BLAST score 558
 E value 2.0e-57
 Match length 107
 % identity 96
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
 construct]

Seq. No. 398321
 Seq. ID LIB3431-013-P1-K1-E10
 Method BLASTX
 NCBI GI g3126854
 BLAST score 705
 E value 1.0e-74
 Match length 133
 % identity 99
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 398322
 Seq. ID LIB3431-013-P1-K1-E11
 Method BLASTX
 NCBI GI g115787
 BLAST score 699
 E value 6.0e-74

activase [Oryza sativa]

Seq. No. 398332
 Seq. ID LIB3431-013-P1-K1-F2
 Method BLASTX
 NCBI GI g2290681
 BLAST score 178
 E value 7.0e-25
 Match length 145
 % identity 46
 NCBI Description (AF000135) acidic cellulase [Citrus sinensis]

Seq. No. 398333
 Seq. ID LIB3431-013-P1-K1-F3
 Method BLASTX
 NCBI GI g1777312
 BLAST score 382
 E value 8.0e-37
 Match length 108
 % identity 66
 NCBI Description (D30622) novel serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 398334
 Seq. ID LIB3431-013-P1-K1-F7
 Method BLASTX
 NCBI GI g1729971
 BLAST score 327
 E value 2.0e-30
 Match length 99
 % identity 69
 NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP) (AQUAPORIN-TIP) >gi_1076745_pir_S52004 gamma-Tip protein - rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza sativa]

Seq. No. 398335
 Seq. ID LIB3431-013-P1-K1-F8
 Method BLASTX
 NCBI GI g4079798
 BLAST score 293
 E value 2.0e-26
 Match length 104
 % identity 59
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 398336
 Seq. ID LIB3431-013-P1-K1-G1
 Method BLASTX
 NCBI GI g2072555
 BLAST score 228
 E value 1.0e-18
 Match length 44
 % identity 98
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 398337
 Seq. ID LIB3431-013-P1-K1-G3
 Method BLASTX
 NCBI GI g347451
 BLAST score 536
 E value 7.0e-55
 Match length 117
 % identity 86
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 398338
 Seq. ID LIB3431-013-P1-K1-G4
 Method BLASTX
 NCBI GI g132105
 BLAST score 665
 E value 6.0e-70
 Match length 144
 % identity 88
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 398339
 Seq. ID LIB3431-013-P1-K1-G6
 Method BLASTN
 NCBI GI g20262
 BLAST score 157
 E value 4.0e-83
 Match length 187
 % identity 96
 NCBI Description O.sativa light-induced mRNA

Seq. No. 398340
 Seq. ID LIB3431-013-P1-K1-G8
 Method BLASTX
 NCBI GI g729668
 BLAST score 245
 E value 6.0e-21
 Match length 83
 % identity 55
 NCBI Description HISTONE H1 >gi_2147479_pir_S65059 histone H1, drought-inducible - Lycopersicon pennellii >gi_436823 (U01890) Solanum pennellii histone H1 [Solanum pennellii]

Seq. No. 398341
 Seq. ID LIB3431-013-P1-K1-G9
 Method BLASTX
 NCBI GI g4469021

BLAST score 245
 E value 1.0e-20
 Match length 72
 % identity 69
 NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No. 398342
 Seq. ID LIB3431-013-P1-K1-H1
 Method BLASTN
 NCBI GI g3041776
 BLAST score 60
 E value 2.0e-25
 Match length 88
 % identity 92
 NCBI Description Oryza sativa mRNA for fructose-1,6-bisphosphatase (plastidic isoform), complete cds

Seq. No. 398343
 Seq. ID LIB3431-013-P1-K1-H11
 Method BLASTX
 NCBI GI g3789954
 BLAST score 368
 E value 4.0e-35
 Match length 110
 % identity 68
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 398344
 Seq. ID LIB3431-013-P1-K1-H12
 Method BLASTX
 NCBI GI g4079798
 BLAST score 376
 E value 5.0e-36
 Match length 125
 % identity 62
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 398345
 Seq. ID LIB3431-013-P1-K1-H3
 Method BLASTN
 NCBI GI g2072554
 BLAST score 102
 E value 2.0e-50
 Match length 118
 % identity 97
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 398346
 Seq. ID LIB3431-013-P1-K1-H5
 Method BLASTX
 NCBI GI g2586083
 BLAST score 206
 E value 2.0e-17
 Match length 117

0664016 1101000

0664016 110100

0664016 110100

0664016 110100

0664016 110100

000101 9104360

Seq. ID LIB3431-014-P1-K1-A6
 Method BLASTX
 NCBI GI g3913018
 BLAST score 321
 E value 7.0e-30
 Match length 80
 % identity 84
 NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
 (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic
 aldolase [Oryza sativa]

Seq. No. 398352
 Seq. ID LIB3431-014-P1-K1-A7
 Method BLASTX
 NCBI GI g3551958
 BLAST score 267
 E value 1.0e-25
 Match length 87
 % identity 71
 NCBI Description (AF082032) senescence-associated protein 12 [Hemerocallis
 hybrid cultivar]

Seq. No. 398353
 Seq. ID LIB3431-014-P1-K1-A8
 Method BLASTX
 NCBI GI g3158476
 BLAST score 348
 E value 6.0e-33
 Match length 93
 % identity 69
 NCBI Description (AF067185) aquaporin 2 [Samanea saman]

Seq. No. 398354
 Seq. ID LIB3431-014-P1-K1-B10
 Method BLASTX
 NCBI GI g132105
 BLAST score 505
 E value 3.0e-51
 Match length 110
 % identity 85
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 398355
 Seq. ID LIB3431-014-P1-K1-B11
 Method BLASTX
 NCBI GI g4559339
 BLAST score 610
 E value 1.0e-63
 Match length 138

% identity 86
 NCBI Description (AC007087) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No. 398356
 Seq. ID LIB3431-014-P1-K1-B12
 Method BLASTX
 NCBI GI g1001794
 BLAST score 161
 E value 4.0e-11
 Match length 41
 % identity 71
 NCBI Description (D64005) hypothetical protein [Synechocystis sp.]

Seq. No. 398357
 Seq. ID LIB3431-014-P1-K1-B2
 Method BLASTN
 NCBI GI g5478796
 BLAST score 57
 E value 1.0e-23
 Match length 73
 % identity 96
 NCBI Description Oryza sativa CAO mRNA for chlorophyll b synthase, partial cds

Seq. No. 398358
 Seq. ID LIB3431-014-P1-K1-B3
 Method BLASTN
 NCBI GI g19094
 BLAST score 46
 E value 6.0e-17
 Match length 54
 % identity 96
 NCBI Description H.vulgare mRNA PsaN for photosystem I subunit N

Seq. No. 398359
 Seq. ID LIB3431-014-P1-K1-B6
 Method BLASTX
 NCBI GI g4741205
 BLAST score 395
 E value 2.0e-38
 Match length 107
 % identity 64
 NCBI Description (AL049746) putative protein [Arabidopsis thaliana]

Seq. No. 398360
 Seq. ID LIB3431-014-P1-K1-B8
 Method BLASTX
 NCBI GI g1262849
 BLAST score 266
 E value 1.0e-25
 Match length 64
 % identity 95
 NCBI Description (U51633) type 1 light-harvesting chlorophyll a/b-binding polypeptide [Pinus palustris]

Seq. No. 398361

09684015 101000

Seq. ID LIB3431-014-P1-K1-C1
Method BLASTN
NCBI GI g3063523
BLAST score 45
E value 6.0e-17
Match length 49
% identity 98
NCBI Description Oryza sativa ribulose 1,5-bisphosphate carboxylase small subunit mRNA, complete cds

Seq. No. 398362
Seq. ID LIB3431-014-P1-K1-C10
Method BLASTN
NCBI GI g3885891
BLAST score 41
E value 5.0e-14
Match length 85
% identity 87
NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds

Seq. No. 398363
Seq. ID LIB3431-014-P1-K1-C11
Method BLASTX
NCBI GI g3122914
BLAST score 213
E value 6.0e-17
Match length 147
% identity 31
NCBI Description VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS)
>gi_1890130_gb_AAB49704.1_ (U89986) valyl tRNA synthetase
[Arabidopsis thaliana]

Seq. No. 398364
Seq. ID LIB3431-014-P1-K1-C2
Method BLASTX
NCBI GI g3126854
BLAST score 609
E value 2.0e-63
Match length 119
% identity 96
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 398365
Seq. ID LIB3431-014-P1-K1-C7
Method BLASTN
NCBI GI g3126853
BLAST score 172
E value 7.0e-92
Match length 210
% identity 100
NCBI Description Oryza sativa chlorophyll a/b binding protein (RCABP89) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 398366
Seq. ID LIB3431-014-P1-K1-C8

NCBI GI g3914603
 BLAST score 664
 E value 6.0e-70
 Match length 130
 % identity 97
 NCBI Description RIBULOSE BISPHTOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
 CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414
 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
 activase [Oryza sativa]

Seq. No. 398377
 Seq. ID LIB3431-014-P1-K1-E10
 Method BLASTX
 NCBI GI g3025189
 BLAST score 455
 E value 3.0e-45
 Match length 141
 % identity 61
 NCBI Description HYPOTHETICAL 67.1 KD PROTEIN SLL1770
 >gi_1652753_dbj_BAA17672_ (D90908) ABC1-like [Synechocystis
 sp.]

Seq. No. 398378
 Seq. ID LIB3431-014-P1-K1-E11
 Method BLASTX
 NCBI GI g2894534
 BLAST score 746
 E value 2.0e-79
 Match length 146
 % identity 99
 NCBI Description (AJ224327) aquaporin [Oryza sativa]

Seq. No. 398379
 Seq. ID LIB3431-014-P1-K1-E12
 Method BLASTX
 NCBI GI g3345477
 BLAST score 534
 E value 1.0e-54
 Match length 149
 % identity 70
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 398380
 Seq. ID LIB3431-014-P1-K1-E2
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 398381
 Seq. ID LIB3431-014-P1-K1-E4
 Method BLASTX

NCBI GI g115787
 BLAST score 236
 E value 5.0e-20
 Match length 67
 % identity 81
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 398382
 Seq. ID LIB3431-014-P1-K1-E5
 Method BLASTX
 NCBI GI g3808101
 BLAST score 306
 E value 7.0e-28
 Match length 75
 % identity 85
 NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]

Seq. No. 398383
 Seq. ID LIB3431-014-P1-K1-E6
 Method BLASTX
 NCBI GI g82080
 BLAST score 501
 E value 1.0e-50
 Match length 137
 % identity 69
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf_1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No. 398384
 Seq. ID LIB3431-014-P1-K1-E8
 Method BLASTX
 NCBI GI g2407279
 BLAST score 575
 E value 2.0e-59
 Match length 117
 % identity 93
 NCBI Description (AF017362) aldolase [Oryza sativa]

Seq. No. 398385
 Seq. ID LIB3431-014-P1-K1-E9
 Method BLASTX
 NCBI GI g2982362
 BLAST score 479
 E value 4.0e-48
 Match length 103
 % identity 85
 NCBI Description (AF053311) glutathione peroxidase [Zantedeschia aethiopica]

Seq. No. 398386
 Seq. ID LIB3431-014-P1-K1-F1
 Method BLASTX
 NCBI GI g548605

BLAST score 608
 E value 3.0e-63
 Match length 133
 % identity 91
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
 (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
 >gi_539055_pir_A48527 photosystem I protein psaK precursor
 - barley >gi_304220 (L12707) photosystem I PSI-K subunit
 [Hordeum vulgare]

Seq. No. 398387
 Seq. ID LIB3431-014-P1-K1-F10
 Method BLASTX
 NCBI GI g3548815
 BLAST score 254
 E value 1.0e-21
 Match length 109
 % identity 50
 NCBI Description (AC005313) similar to axoneme-associated protein mst101
 [Arabidopsis thaliana]

Seq. No. 398388
 Seq. ID LIB3431-014-P1-K1-F11
 Method BLASTX
 NCBI GI g1903364
 BLAST score 296
 E value 1.0e-26
 Match length 145
 % identity 43
 NCBI Description (AC000104) EST gb_T45093 comes from this gene. [Arabidopsis
 thaliana]

Seq. No. 398389
 Seq. ID LIB3431-014-P1-K1-F2
 Method BLASTX
 NCBI GI g3738285
 BLAST score 320
 E value 2.0e-29
 Match length 101
 % identity 61
 NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 398390
 Seq. ID LIB3431-014-P1-K1-F4
 Method BLASTX
 NCBI GI g3548815
 BLAST score 255
 E value 6.0e-22
 Match length 105
 % identity 48
 NCBI Description (AC005313) similar to axoneme-associated protein mst101
 [Arabidopsis thaliana]

Seq. No. 398391
 Seq. ID LIB3431-014-P1-K1-F6
 Method BLASTX
 NCBI GI g1346771

Seq. ID LIB3431-014-P1-K1-H1
 Method BLASTX
 NCBI GI g729477
 BLAST score 331
 E value 9.0e-31
 Match length 133
 % identity 50
 NCBI Description FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR)
 >gi_320548_pir_A44974 ferredoxin--NADP+ reductase (EC
 1.18.1.2) precursor - common ice plant >gi_167256 (M25528)
 ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1)
 [Mesembryanthemum crystallinum] >gi_226768_prf_1604475A
 ferredoxin NADP reductase [Mesembryanthemum crystallinum]

Seq. No. 398402
 Seq. ID LIB3431-014-P1-K1-H11
 Method BLASTX
 NCBI GI g266893
 BLAST score 768
 E value 5.0e-82
 Match length 151
 % identity 96
 NCBI Description RIBULOSE BISPHTHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
 CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
 >gi_322416_pir_S28172 ribulose-bisphosphate carboxylase
 activase - cucumber >gi_18284_emb_CAA47906_ (X67674)
 rubisco activase [Cucumis sativus]

Seq. No. 398403
 Seq. ID LIB3431-014-P1-K1-H3
 Method BLASTN
 NCBI GI g3075487
 BLAST score 281
 E value 1.0e-157
 Match length 285
 % identity 100
 NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69)
 mRNA, complete cds

Seq. No. 398404
 Seq. ID LIB3431-014-P1-K1-H4
 Method BLASTX
 NCBI GI g4056507
 BLAST score 267
 E value 3.0e-23
 Match length 85
 % identity 62
 NCBI Description (AC005896) putative RNA binding protein [Arabidopsis
 thaliana]

Seq. No. 398405
 Seq. ID LIB3431-014-P1-K1-H5
 Method BLASTX
 NCBI GI g320618
 BLAST score 635
 E value 2.0e-66
 Match length 138

E value 5.0e-28
Match length 80
% identity 98
NCBI Description Oryza sativa gene for cytoplasmic aldolase, complete cds,
clone:Aldp

Seq. No. 398411
Seq. ID LIB3431-014-P1-N1-B10
Method BLASTX
NCBI GI g347451
BLAST score 207
E value 2.0e-16
Match length 39
% identity 100
NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
sativa]

Seq. No. 398412
Seq. ID LIB3431-014-P1-N1-B12
Method BLASTX
NCBI GI g1001794
BLAST score 168
E value 6.0e-12
Match length 41
% identity 73
NCBI Description (D64005) hypothetical protein [Synechocystis sp.]

Seq. No. 398413
Seq. ID LIB3431-014-P1-N1-B3
Method BLASTX
NCBI GI g3914466
BLAST score 302
E value 2.0e-27
Match length 71
% identity 79
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
(PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN
subunit precursor [Zea mays]

Seq. No. 398414
Seq. ID LIB3431-014-P1-N1-B8
Method BLASTN
NCBI GI g20181
BLAST score 138
E value 1.0e-71
Match length 145
% identity 99
NCBI Description Rice cab2R gene for light harvesting chlorophyll
a/b-binding protein

Seq. No. 398415
Seq. ID LIB3431-014-P1-N1-C1
Method BLASTN
NCBI GI g218207
BLAST score 94
E value 1.0e-45
Match length 138

% identity 92
 NCBI Description Oryza sativa mRNA for the small subunit of
 ribulose-1,5-bisphosphate carboxylase, complete cds, clone
 pOSSS1139

Seq. No. 398416
 Seq. ID LIB3431-014-P1-N1-C10
 Method BLASTX
 NCBI GI g3885892
 BLAST score 342
 E value 4.0e-32
 Match length 66
 % identity 100
 NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 398417
 Seq. ID LIB3431-014-P1-N1-C2
 Method BLASTX
 NCBI GI g3126854
 BLAST score 272
 E value 6.0e-24
 Match length 57
 % identity 93
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 398418
 Seq. ID LIB3431-014-P1-N1-C7
 Method BLASTN
 NCBI GI g3126853
 BLAST score 145
 E value 8.0e-76
 Match length 207
 % identity 97
 NCBI Description Oryza sativa chlorophyll a/b binding protein (RCABP89)
 mRNA, nuclear gene encoding chloroplast protein, complete
 cds

Seq. No. 398419
 Seq. ID LIB3431-014-P1-N1-C8
 Method BLASTX
 NCBI GI g3126854
 BLAST score 456
 E value 9.0e-46
 Match length 103
 % identity 94
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 398420
 Seq. ID LIB3431-014-P1-N1-D10
 Method BLASTX
 NCBI GI g1835731
 BLAST score 236
 E value 6.0e-20
 Match length 56
 % identity 82
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 398421
 Seq. ID LIB3431-014-P1-N1-D11
 Method BLASTX
 NCBI GI g733454
 BLAST score 210
 E value 1.0e-16
 Match length 48
 % identity 85
 NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No. 398422
 Seq. ID LIB3431-014-P1-N1-D3
 Method BLASTX
 NCBI GI g99486
 BLAST score 275
 E value 4.0e-24
 Match length 67
 % identity 79
 NCBI Description chlorophyll a/b-binding protein (clone pINEab 31) - Scotch pine >gi_20792_emb_CAA41406_ (X58516) Type II chlorophyll a/b-binding protein [Pinus sylvestris]

Seq. No. 398423
 Seq. ID LIB3431-014-P1-N1-D6
 Method BLASTN
 NCBI GI g168525
 BLAST score 37
 E value 3.0e-11
 Match length 53
 % identity 92
 NCBI Description Zea mays nucleic acid-binding protein (NBP)

Seq. No. 398424
 Seq. ID LIB3431-014-P1-N1-D8
 Method BLASTX
 NCBI GI g80783
 BLAST score 190
 E value 3.0e-14
 Match length 120
 % identity 36
 NCBI Description hypothetical 31.7K protein (aphE region) - Streptomyces griseus >gi_153164 (M37378) streptomycin-3'-phosphotransferase [Streptomyces griseus]

Seq. No. 398425
 Seq. ID LIB3431-014-P1-N1-D9
 Method BLASTX
 NCBI GI g671740
 BLAST score 225
 E value 2.0e-18
 Match length 44
 % identity 98
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 398426

Seq. ID LIB3431-014-P1-N1-E1
 Method BLASTX
 NCBI GI g132166
 BLAST score 149
 E value 1.0e-09
 Match length 31
 % identity 81
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
 CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
 >gi_81660_pir_S04048 ribulose-bisphosphate carboxylase
 activase precursor - Arabidopsis thaliana
 >gi_16471_emb_CAA32429 (X14212) rubisco activase (AA 1 -
 473) [Arabidopsis thaliana]

Seq. No. 398427
 Seq. ID LIB3431-014-P1-N1-E11
 Method BLASTX
 NCBI GI g2696804
 BLAST score 308
 E value 4.0e-28
 Match length 56
 % identity 100
 NCBI Description (AB009665) water channel protein [Oryza sativa]

Seq. No. 398428
 Seq. ID LIB3431-014-P1-N1-E12
 Method BLASTN
 NCBI GI g606816
 BLAST score 350
 E value 0.0e+00
 Match length 364
 % identity 99
 NCBI Description Oryza sativa chloroplast carbonic anhydrase mRNA, complete
 cds

Seq. No. 398429
 Seq. ID LIB3431-014-P1-N1-E2
 Method BLASTN
 NCBI GI g2072554
 BLAST score 343
 E value 0.0e+00
 Match length 377
 % identity 98
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
 cds

Seq. No. 398430
 Seq. ID LIB3431-014-P1-N1-E4
 Method BLASTX
 NCBI GI g3036951
 BLAST score 233
 E value 2.0e-19
 Match length 57
 % identity 93
 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein
 [Nicotiana glauca]

Seq. No. 398431
 Seq. ID LIB3431-014-P1-N1-E5
 Method BLASTX
 NCBI GI g3808101
 BLAST score 181
 E value 2.0e-13
 Match length 43
 % identity 84
 NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]

Seq. No. 398432
 Seq. ID LIB3431-014-P1-N1-E8
 Method BLASTX
 NCBI GI g2407279
 BLAST score 200
 E value 8.0e-25
 Match length 67
 % identity 93
 NCBI Description (AF017362) aldolase [Oryza sativa]

Seq. No. 398433
 Seq. ID LIB3431-014-P1-N1-E9
 Method BLASTX
 NCBI GI g2982362
 BLAST score 494
 E value 6.0e-50
 Match length 100
 % identity 89
 NCBI Description (AF053311) glutathione peroxidase [Zantedeschia aethiopica]

Seq. No. 398434
 Seq. ID LIB3431-014-P1-N1-F1
 Method BLASTX
 NCBI GI g548605
 BLAST score 232
 E value 1.0e-20
 Match length 64
 % identity 88
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
 (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
 >gi_539055_pir_A48527 photosystem I protein psaK precursor
 - barley >gi_304220 (L12707) photosystem I PSI-K subunit
 [Hordeum vulgare]

Seq. No. 398435
 Seq. ID LIB3431-014-P1-N1-F5
 Method BLASTN
 NCBI GI g11957
 BLAST score 63
 E value 7.0e-27
 Match length 143
 % identity 43
 NCBI Description Rice complete chloroplast genome

Seq. No. 398436
 Seq. ID LIB3431-014-P1-N1-F6
 Method BLASTX

NCBI GI g1346771
 BLAST score 189
 E value 2.0e-17
 Match length 67
 % identity 78
 NCBI Description PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP]
 >gi_1086117_pir_S52988 phosphoenolpyruvate carboxykinase
 (PCK1) - Urochloa panicoides >gi_607752 (U09241)
 phosphoenolpyruvate carboxykinase [Urochloa panicoides]

Seq. No. 398437
 Seq. ID LIB3431-014-P1-N1-F9
 Method BLASTX
 NCBI GI g3789954
 BLAST score 277
 E value 2.0e-24
 Match length 54
 % identity 94
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 398438
 Seq. ID LIB3431-014-P1-N1-G2
 Method BLASTX
 NCBI GI g2407279
 BLAST score 149
 E value 2.0e-11
 Match length 45
 % identity 81
 NCBI Description (AF017362) aldolase [Oryza sativa]

Seq. No. 398439
 Seq. ID LIB3431-014-P1-N1-G4
 Method BLASTN
 NCBI GI g20262
 BLAST score 300
 E value 1.0e-168
 Match length 345
 % identity 97
 NCBI Description O.sativa light-induced mRNA

Seq. No. 398440
 Seq. ID LIB3431-014-P1-N1-G6
 Method BLASTN
 NCBI GI g3789949
 BLAST score 142
 E value 2.0e-74
 Match length 146
 % identity 99
 NCBI Description Oryza sativa translation initiation factor (GOS2) mRNA, complete cds

Seq. No. 398441
 Seq. ID LIB3431-014-P1-N1-G7
 Method BLASTX
 NCBI GI g283039
 BLAST score 157

E value 2.0e-10
 Match length 39
 % identity 79
 NCBI Description gene iojap protein - maize >gi_22349_emb_CAA78772_ (Z15063)
 putative iojap protein [Zea mays]

Seq. No. 398442
 Seq. ID LIB3431-014-P1-N1-H1
 Method BLASTX
 NCBI GI g729478
 BLAST score 247
 E value 1.0e-23
 Match length 60
 % identity 83
 NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
 >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
 reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_
 (AP000616) ESTs AU078647(E1557), C72400(E1557) correspond to
 a region of the predicted gene.; similar to
 ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

Seq. No. 398443
 Seq. ID LIB3431-014-P1-N1-H3
 Method BLASTN
 NCBI GI g3075487
 BLAST score 80
 E value 5.0e-37
 Match length 205
 % identity 90
 NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69)
 mRNA, complete cds

Seq. No. 398444
 Seq. ID LIB3431-014-P1-N1-H8
 Method BLASTX
 NCBI GI g4666287
 BLAST score 336
 E value 1.0e-31
 Match length 65
 % identity 100
 NCBI Description (D85764) cytosolic monodehydroascorbate reductase [Oryza
 sativa]

Seq. No. 398445
 Seq. ID LIB3431-014-P1-N1-H9
 Method BLASTN
 NCBI GI g3075487
 BLAST score 241
 E value 1.0e-133
 Match length 253
 % identity 99
 NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69)
 mRNA, complete cds

Seq. No. 398446
 Seq. ID LIB3431-015-P1-K1-A10
 Method BLASTX

0001015 101000

NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 398472
Seq. ID LIB3431-015-P1-K1-D5
Method BLASTX
NCBI GI g2196672
BLAST score 444
E value 4.0e-44
Match length 93
% identity 89
NCBI Description (Y08807) HMGd1 [Zea mays]

Seq. No. 398473
Seq. ID LIB3431-015-P1-K1-D7
Method BLASTX
NCBI GI g4455180
BLAST score 184
E value 1.0e-13
Match length 44
% identity 82
NCBI Description (AL035521) putative protein [Arabidopsis thaliana]

Seq. No. 398474
Seq. ID LIB3431-015-P1-K1-D9
Method BLASTX
NCBI GI g3885888
BLAST score 282
E value 3.0e-25
Match length 63
% identity 90
NCBI Description (AF093632) high mobility group protein [Oryza sativa]

Seq. No. 398475
Seq. ID LIB3431-015-P1-K1-E1
Method BLASTN
NCBI GI g295500
BLAST score 50
E value 4.0e-19
Match length 102
% identity 87
NCBI Description Triticum aestivum heat shock protein 16.9C (hsp16.9C) mRNA, 3' end

Seq. No. 398476
Seq. ID LIB3431-015-P1-K1-E11
Method BLASTN
NCBI GI g6015437
BLAST score 37
E value 3.0e-11
Match length 48
% identity 66
NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 398477
Seq. ID LIB3431-015-P1-K1-E12
Method BLASTN

[Arabidopsis thaliana]

Seq. No. 398483
 Seq. ID LIB3431-015-P1-K1-F10
 Method BLASTX
 NCBI GI g399213
 BLAST score 501
 E value 6.0e-51
 Match length 119
 % identity 82
 NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG
 CD4B PRECURSOR >gi_100190_pir_B35905 CD4B protein - tomato
 >gi_170435 (M32604) ATP-dependent protease (CD4B)
 [Lycopersicon esculentum]

Seq. No. 398484
 Seq. ID LIB3431-015-P1-K1-F11
 Method BLASTX
 NCBI GI g3128228
 BLAST score 520
 E value 1.0e-54
 Match length 124
 % identity 88
 NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis
 thaliana] >gi_3337376 (AC004481) putative ribosomal protein
 L18A [Arabidopsis thaliana]

Seq. No. 398485
 Seq. ID LIB3431-015-P1-K1-F2
 Method BLASTX
 NCBI GI g2497903
 BLAST score 220
 E value 6.0e-18
 Match length 59
 % identity 68
 NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2
 >gi_1752831_dbj_BAA14038.1 (D89931) metallothionein-like
 protein [Oryza sativa] >gi_1815628 (U43530)
 metallothionein-like type 2 [Oryza sativa]

Seq. No. 398486
 Seq. ID LIB3431-015-P1-K1-F3
 Method BLASTX
 NCBI GI g115787
 BLAST score 578
 E value 6.0e-60
 Match length 112
 % identity 98
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
 protein 2R precursor - rice >gi_20182_emb_CAA32109
 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
 [Oryza sativa]

Seq. No. 398487
 Seq. ID LIB3431-015-P1-K1-F4
 Method BLASTX

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Seq. No. 398503
 Seq. ID LIB3431-015-P1-K1-H2
 Method BLASTX
 NCBI GI g4455180
 BLAST score 396
 E value 1.0e-38
 Match length 108
 % identity 71
 NCBI Description (AL035521) putative protein [Arabidopsis thaliana]

Seq. No. 398504
 Seq. ID LIB3431-015-P1-K1-H3
 Method BLASTX
 NCBI GI g3913811
 BLAST score 704
 E value 1.0e-74
 Match length 141
 % identity 99
 NCBI Description GLUTAMYL-TRNA REDUCTASE PRECURSOR (GLUTR)
 >gi_2920320_dbj_BAA25003_ (AB011416) glutamyl-tRNA
 reductase [Oryza sativa]

Seq. No. 398505
 Seq. ID LIB3431-015-P1-K1-H6
 Method BLASTN
 NCBI GI g2072554
 BLAST score 212
 E value 1.0e-116
 Match length 260
 % identity 96
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
 cds

Seq. No. 398506
 Seq. ID LIB3431-015-P1-K1-H7
 Method BLASTX
 NCBI GI g3075488
 BLAST score 211
 E value 6.0e-17
 Match length 57
 % identity 72
 NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 398507
 Seq. ID LIB3431-015-P1-K1-H8
 Method BLASTX
 NCBI GI g3915309
 BLAST score 159
 E value 9.0e-11
 Match length 93
 % identity 32
 NCBI Description D-XYLOSE-PROTON SYMPORT (D-XYLOSE TRANSPORTER) >gi_2895856
 (AF045552) D-xylose proton-symporter [Lactobacillus brevis]

Seq. No. 398508
 Seq. ID LIB3431-015-P1-K1-H9

Match length 43
% identity 100
NCBI Description Rice cablR gene for light harvesting chlorophyll
a/b-binding protein

Seq. No. 398540
Seq. ID LIB3431-016-P1-K1-D11
Method BLASTX
NCBI GI g4914457
BLAST score 303
E value 1.0e-27
Match length 105
% identity 52
NCBI Description (AL050400) putative protein [Arabidopsis thaliana]

Seq. No. 398541
Seq. ID LIB3431-016-P1-K1-D12
Method BLASTX
NCBI GI g927025
BLAST score 196
E value 5.0e-15
Match length 116
% identity 38
NCBI Description (L44134) SPF1-like DNA-binding protein [Cucumis sativus]

Seq. No. 398542
Seq. ID LIB3431-016-P1-K1-D2
Method BLASTX
NCBI GI g2129950
BLAST score 646
E value 8.0e-68
Match length 132
% identity 98
NCBI Description inorganic pyrophosphatase (EC 3.6.1.1) (clone TVP9) -
common tobacco

Seq. No. 398543
Seq. ID LIB3431-016-P1-K1-D4
Method BLASTX
NCBI GI g115813
BLAST score 423
E value 1.0e-41
Match length 117
% identity 73
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
CAB-8) >gi_19182_emb_CAA33330_(X15258) Type III
chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 398544
Seq. ID LIB3431-016-P1-K1-D6
Method BLASTX
NCBI GI g3789954
BLAST score 743
E value 4.0e-79
Match length 134
% identity 100
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza

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Seq. No.      398546
Seq. ID      LIB3431-016-P1-K1-D9
Method       BLASTX
NCBI GI      g2245136
BLAST score   289
E value      6.0e-26
Match length  92
% identity    62
NCBI Description (Z97344) trehalose-6-phosphate synthase like protein
               [Arabidopsis thaliana]
```

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Seq. No.      398548
Seq. ID       LIB3431-016-P1-K1-E11
Method        BLASTX
NCBI GI       g132105
BLAST score    715
E value       7.0e-76
Match length   132
% identity     99
NCBI Description  RIBULOSE BIPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose biphosphate
                  carboxylase S [Oryza sativa]

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E value 3.0e-11
Match length 57
% identity 91
NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence

Seq. No. 398555
Seq. ID LIB3431-016-P1-K1-F10
Method BLASTX
NCBI GI g730456
BLAST score 569
E value 9.0e-59
Match length 108
% identity 99
NCBI Description 40S RIBOSOMAL PROTEIN S19

Seq. No. 398556
Seq. ID LIB3431-016-P1-K1-F2
Method BLASTX
NCBI GI g2493318
BLAST score 171
E value 4.0e-12
Match length 72
% identity 46
NCBI Description BLUE COPPER PROTEIN PRECURSOR >gi_562779_emb_CAA80963_
(Z25471) blue copper protein [Pisum sativum]
>gi_1098264_prf_2115352A blue Cu protein [Pisum sativum]

Seq. No. 398557
Seq. ID LIB3431-016-P1-K1-F5
Method BLASTX
NCBI GI g2072555
BLAST score 232
E value 7.0e-20
Match length 44
% identity 98
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
protein [Oryza sativa]

Seq. No. 398558
Seq. ID LIB3431-016-P1-K1-F7
Method BLASTX
NCBI GI g1707998
BLAST score 262
E value 2.0e-23
Match length 52
% identity 98
NCBI Description SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR
(SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
(SHMT) >gi_481944_pir_S40218 glycine
hydroxymethyltransferase (EC 2.1.2.1) - potato
>gi_438247_emb_CAA81082_ (Z25863) glycine
hydroxymethyltransferase [Solanum tuberosum]

Seq. No. 398559
Seq. ID LIB3431-016-P1-K1-F8
Method BLASTX

000101-9103960

NCBI GI g4220481
BLAST score 205
E value 4.0e-16
Match length 107
% identity 43
NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 398560
Seq. ID LIB3431-016-P1-K1-G1
Method BLASTX
NCBI GI g115787
BLAST score 695
E value 2.0e-73
Match length 134
% identity 99
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 398561
Seq. ID LIB3431-016-P1-K1-G10
Method BLASTX
NCBI GI g4455323
BLAST score 397
E value 1.0e-38
Match length 136
% identity 59
NCBI Description (AL035525) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No. 398562
Seq. ID LIB3431-016-P1-K1-G11
Method BLASTX
NCBI GI g462195
BLAST score 423
E value 1.0e-41
Match length 88
% identity 91
NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_100682_pir_S21636 GOS2 protein - rice >gi_20238_emb_CAA36190 (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No. 398563
Seq. ID LIB3431-016-P1-K1-G12
Method BLASTX
NCBI GI g2501189
BLAST score 402
E value 3.0e-39
Match length 111
% identity 72
NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR >gi_2130146_pir_S61419 thiamine biosynthetic enzyme thil-1 - maize >gi_596078 (U17350) thiamine biosynthetic enzyme

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[Zea mays]

Seq. No. 398564
 Seq. ID LIB3431-016-P1-K1-G3
 Method BLASTX
 NCBI GI g115787
 BLAST score 554
 E value 6.0e-57
 Match length 125
 % identity 87
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 398565
 Seq. ID LIB3431-016-P1-K1-G4
 Method BLASTX
 NCBI GI g710308
 BLAST score 268
 E value 1.0e-23
 Match length 49
 % identity 96
 NCBI Description (U11693) victorin binding protein [Avena sativa]

Seq. No. 398566
 Seq. ID LIB3431-016-P1-K1-G5
 Method BLASTX
 NCBI GI g2570511
 BLAST score 590
 E value 3.0e-61
 Match length 111
 % identity 99
 NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No. 398567
 Seq. ID LIB3431-016-P1-K1-G6
 Method BLASTX
 NCBI GI g3789954
 BLAST score 515
 E value 2.0e-52
 Match length 96
 % identity 100
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 398568
 Seq. ID LIB3431-016-P1-K1-G7
 Method BLASTX
 NCBI GI g1899188
 BLAST score 359
 E value 4.0e-34
 Match length 132
 % identity 55
 NCBI Description (U90212) DNA binding protein ACBF [Nicotiana tabacum]

Seq. No.	398569
Seq. ID	LIB3431-016-P1-K1-G8
Method	BLASTX
NCBI GI	g556409
BLAST score	366
E value	6.0e-35
Match length	112
% identity	72
NCBI Description	(L34551) transcriptional activator protein [Oryza sativa]

Seq. No.	398570
Seq. ID	LIB3431-016-P1-K1-G9
Method	BLASTX
NCBI GI	g4886307
BLAST score	662
E value	1.0e-69
Match length	133
% identity	92
NCBI Description	(AJ242588) 1-deoxy-d-xylulose-5-phosphate reductoisomerase [Arabidopsis thaliana]

Seq. No.	398571
Seq. ID	LIB3431-016-P1-K1-H1
Method	BLASTX
NCBI GI	g1778149
BLAST score	563
E value	4.0e-58
Match length	119
% identity	93
NCBI Description	(U66404) phosphate/phosphoenolpyruvate translocator precursor [Zea mays]

```
Seq. No.      398572
Seq. ID      LIB3431-016-P1-K1-H12
Method       BLASTX
NCBI GI      g3868758
BLAST score   370
E value      2.0e-35
Match length  92
% identity    77
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
```

```
Seq. No.      398573
Seq. ID      LIB3431-016-P1-K1-H2
Method       BLASTX
NCBI GI      g5306269
BLAST score   256
E value      5.0e-22
Match length  128
% identity    25
NCBI Description (AC006233) unknown protein [Arabidopsis thaliana]
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```
Seq. No.      398574
Seq. ID      LIB3431-016-P1-K1-H3
Method       BLASTX
NCBI GI      g451193
BLAST score  442
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Seq. No. 398588
 Seq. ID LIB3431-017-P1-K1-A9
 Method BLASTX
 NCBI GI g4337192
 BLAST score 292
 E value 3.0e-26
 Match length 90
 % identity 66
 NCBI Description (AC006403) hypothetical protein [Arabidopsis thaliana]

Seq. No. 398589
 Seq. ID LIB3431-017-P1-K1-B1
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 398590
 Seq. ID LIB3431-017-P1-K1-B10
 Method BLASTX
 NCBI GI g733454
 BLAST score 589
 E value 4.0e-61
 Match length 124
 % identity 87
 NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No. 398591
 Seq. ID LIB3431-017-P1-K1-B11
 Method BLASTX
 NCBI GI g542200
 BLAST score 263
 E value 7.0e-23
 Match length 98
 % identity 56
 NCBI Description hypothetical protein - garden asparagus
 >gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus officinalis]

Seq. No. 398592
 Seq. ID LIB3431-017-P1-K1-B2
 Method BLASTN
 NCBI GI g21843
 BLAST score 96
 E value 2.0e-46
 Match length 312
 % identity 87
 NCBI Description Wheat PsbO mRNA for 33kDa oxygen evolving protein of photosystem II

Seq. No.	398593
Seq. ID	LIB3431-017-P1-K1-B3
Method	BLASTX
NCBI GI	g2618704
BLAST score	619
E value	1.0e-64
Match length	136
% identity	85
NCBI Description	(AC002510) putative thioredoxin reductase [Arabidopsis thaliana]

```
Seq. No.      398594
Seq. ID       LIB3431-017-P1-K1-B4
Method        BLASTX
NCBI GI       g129233
BLAST score    491
E value       1.0e-49
Match length  120
% identity     82
NCBI Description ORYZAIN GAMMA CHAIN PRECURSOR >gi_67646_pir__KHRZOG oryzain
(EC 3.4.22.-) gamma precursor - rice
>gi_218185_dbj_BAA14404_ (D90408) oryzain gamma precursor
[Oryza sativa]
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```
Seq. No.      398595
Seq. ID       LIB3431-017-P1-K1-B5
Method        BLASTX
NCBI GI       g5541681
BLAST score   363
E value       1.0e-34
Match length  133
% identity    59
NCBI Description (AL096859) putative protein [Arabidopsis thaliana]
```

Seq. No.	398596
Seq. ID	LIB3431-017-P1-K1-B7
Method	BLASTX
NCBI GI	g120661
BLAST score	228
E value	8.0e-19
Match length	45
% identity	93
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate dehydrogenase A-subunit precursor [Nicotiana tabacum]

```
Seq. No.      398597
Seq. ID       LIB3431-017-P1-K1-C1
Method        BLASTX
NCBI GI       g3184098
BLAST score    355
E value       1.0e-33
Match length   118
% identity     56
NCBI Description (AL023777) coenzyme a synthetase [Schizosaccharomyces pombe]
```

Seq. No. 398598
 Seq. ID LIB3431-017-P1-K1-C10
 Method BLASTX
 NCBI GI g2072727
 BLAST score 699
 E value 5.0e-74
 Match length 140
 % identity 97
 NCBI Description (Y12595) Fd-GOGAT protein [Oryza sativa]

Seq. No. 398599
 Seq. ID LIB3431-017-P1-K1-C11
 Method BLASTX
 NCBI GI g131225
 BLAST score 589
 E value 4.0e-61
 Match length 122
 % identity 93
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 398600
 Seq. ID LIB3431-017-P1-K1-C12
 Method BLASTN
 NCBI GI g3885891
 BLAST score 41
 E value 1.0e-13
 Match length 60
 % identity 93
 NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds

Seq. No. 398601
 Seq. ID LIB3431-017-P1-K1-C2
 Method BLASTX
 NCBI GI g282833
 BLAST score 686
 E value 2.0e-72
 Match length 143
 % identity 97
 NCBI Description phosphoglycerate kinase (EC 2.7.2.3) - spinach (fragment)

Seq. No. 398602
 Seq. ID LIB3431-017-P1-K1-C3
 Method BLASTX
 NCBI GI g585421
 BLAST score 429
 E value 3.0e-42
 Match length 147
 % identity 53
 NCBI Description LIPOXYGENASE, CHLOROPLAST PRECURSOR >gi_541879_pir_JQ2391 lipoxxygenase (EC 1.13.11.12) AtLox2 - Arabidopsis thaliana >gi_431258 (L23968) lipoxxygenase [Arabidopsis thaliana]

Seq. No. 398603

NCBI GI	g4581207
BLAST score	504
E value	4.0e-51
Match length	144
% identity	73
NCBI Description	(Y17914) cyclic nucleotide and calmodulin-regulated ion channel [Arabidopsis thaliana]
Seq. No.	398608
Seq. ID	LIB3431-017-P1-K1-D3
Method	BLASTX
NCBI GI	g3075488
BLAST score	533
E value	2.0e-54
Match length	120
% identity	85
NCBI Description	(AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.	398609
Seq. ID	LIB3431-017-P1-K1-D5
Method	BLASTX
NCBI GI	g3927827
BLAST score	190
E value	3.0e-14
Match length	104
% identity	43
NCBI Description	(AC005727) osmotin-like protein precursor [Arabidopsis thaliana]
Seq. No.	398610
Seq. ID	LIB3431-017-P1-K1-D6
Method	BLASTN
NCBI GI	g11957
BLAST score	292
E value	1.0e-163
Match length	308
% identity	99
NCBI Description	Rice complete chloroplast genome
Seq. No.	398611
Seq. ID	LIB3431-017-P1-K1-D7
Method	BLASTX
NCBI GI	g5902390
BLAST score	386
E value	3.0e-37
Match length	126
% identity	60
NCBI Description	(AC008148) Unknown protein [Arabidopsis thaliana]
Seq. No.	398612
Seq. ID	LIB3431-017-P1-K1-D8
Method	BLASTX
NCBI GI	g400879
BLAST score	211
E value	6.0e-17
Match length	103
% identity	50


```
Method          BLASTX
NCBI GI         g3789952
BLAST score     383
E value        3.0e-37
Match length    85
% identity      98
NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                  sativa]
```

```
Seq. No.          398638
Seq. ID           LIB3431-017-P1-K1-H11
Method            BLASTX
NCBI GI           g5919219
BLAST score       202
E value           1.0e-15
Match length      133
% identity        13
NCBI Description   (AF186273) leucine-rich repeats containing F-box protein
                   FBL3 [Homo sapiens]
```

Seq. No.	398639
Seq. ID	LIB3431-017-P1-K1-H12
Method	BLASTN
NCBI GI	g6015437
BLAST score	33
E value	4.0e-09
Match length	33
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

```
Seq. No.      398640
Seq. ID       LIB3431-017-P1-K1-H2
Method        BLASTX
NCBI GI       g3885892
BLAST score   442
E value       8.0e-44
Match length  85
% identity    98
NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
```

```
Seq. No.      398641
Seq. ID      LIB3431-017-P1-K1-H3
Method       BLASTX
NCBI GI      g3075488
BLAST score   426
E value      6.0e-42
Match length  82
% identity    99
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
```

Seq. No.	398642
Seq. ID	LIB3431-017-P1-K1-H4
Method	BLASTX
NCBI GI	g1173189
BLAST score	220
E value	8.0e-18
Match length	42

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NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_(X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 398648
Seq. ID LIB3431-017-P1-N1-A4
Method BLASTN
NCBI GI g2072554
BLAST score 361
E value 0.0e+00
Match length 369
% identity 99
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 398649
Seq. ID LIB3431-017-P1-N1-A5
Method BLASTX
NCBI GI g347451
BLAST score 365
E value 6.0e-35
Match length 69
% identity 99
NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 398650
Seq. ID LIB3431-017-P1-N1-A7
Method BLASTN
NCBI GI g218209
BLAST score 187
E value 1.0e-101
Match length 235
% identity 95
NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No. 398651
Seq. ID LIB3431-017-P1-N1-A8
Method BLASTN
NCBI GI g886692
BLAST score 377
E value 0.0e+00
Match length 385
% identity 99
NCBI Description O.sativa mRNA for lipid transfer protein, b1

Seq. No. 398652
Seq. ID LIB3431-017-P1-N1-B1
Method BLASTN
NCBI GI g2072554
BLAST score 160
E value 8.0e-85
Match length 244
% identity 91
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

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```
Seq. No.      398654
Seq. ID      LIB3431-017-P1-N1-B2
Method       BLASTX
NCBI GI      g482311
BLAST score   260
E value      1.0e-22
Match length  51
% identity    100
NCBI Description  photosystem II oxygen-evolving complex protein 1 - rice
                  (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
```

```
Seq. No.      398656
Seq. ID      LIB3431-017-P1-N1-B5
Method       BLASTX
NCBI GI      g5541681
BLAST score   182
E value      2.0e-13
Match length  79
% identity    58
NCBI Description (AL096859) putative protein [Arabidopsis thaliana]
```

```
Seq. No.          398657
Seq. ID           LIB3431-017-P1-N1-C1
Method            BLASTX
NCBI GI           g586339
BLAST score       182
E value           2.0e-13
Match length      67
% identity        46
NCBI Description   PEROXISOMAL-COENZYME A SYNTHETASE >gi_626794_pir_S46098
                  probable AMP-binding protein - yeast (Saccharomyces
                  cerevisiae) >gi_536615_emb_CAA85185_(Z36091) ORF YBR222c
```

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```
Seq. No.      398662
Seq. ID      LIB3431-017-P1-N1-C3
Method       BLASTX
NCBI GI      g450231
BLAST score   186
E value      8.0e-14
Match length  56
% identity    59
NCBI Description (U05041) lipoxxygenase [Cuscuta reflexa]
```

```
Seq. No.          398663
Seq. ID           LIB3431-017-P1-N1-C6
Method            BLASTX
NCBI GI           g132105
BLAST score       174
E value           1.0e-20
Match length      57
% identity        95
NCBI Description  RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
```

```
Seq. No.: 398664
Seq. ID LIB3431-017-P1-N1-C7
Method BLASTX
NCBI GI g482311
BLAST score 175
E value 1.0e-12
Match length 34
% identity 100
NCBI Description photosystem II oxygen-evolving complex protein 1 - rice
(strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
complex protein 1 [Oryza sativa]
```

```
Seq. No.      398665
Seq. ID      LIB3431-017-P1-N1-C8
Method       BLASTX
NCBI GI      g4678346
BLAST score   187
E value      5.0e-14
Match length  44
% identity   77
NCBI Description (AL049659) putative protein [Arabidopsis thaliana]
```

```
Seq. No.      398666
Seq. ID      LIB3431-017-P1-N1-C9
Method       BLASTX
NCBI GI      g3341699
BLAST score   238
E value      7.0e-20
Match length  153
% identity    37
NCBI Description (AC003672) putative gibberellin beta-hydroxylase
                [Arabidopsis thaliana]
```

```
Seq. No.      398667
Seq. ID      LIB3431-017-P1-N1-D10
Method       BLASTX
NCBI GI      g462195
BLAST score   234
E value      1.0e-19
```


Seq. No. 398692
Seq. ID LIB3431-017-P1-N1-H2
Method BLASTN
NCBI GI g3885891
BLAST score 207
E value 1.0e-113
Match length 247
% identity 96
NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds

Seq. No. 398693
Seq. ID LIB3431-017-P1-N1-H3
Method BLASTX
NCBI GI g3075488
BLAST score 176
E value 9.0e-13
Match length 33
% identity 100
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 398694
Seq. ID LIB3431-017-P1-N1-H4
Method BLASTN
NCBI GI g2072554
BLAST score 140
E value 7.0e-73
Match length 248
% identity 88
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 398695
Seq. ID LIB3431-017-P1-N1-H5
Method BLASTN
NCBI GI g4105560
BLAST score 141
E value 2.0e-73
Match length 190
% identity 94
NCBI Description Oryza sativa ribulose-5-phosphate-3-epimerase (RPE) mRNA, complete cds

Seq. No. 398696
Seq. ID LIB3431-017-P1-N1-H7
Method BLASTX
NCBI GI g4126473
BLAST score 195
E value 5.0e-15
Match length 47
% identity 81
NCBI Description (AB014884) adenylyl cyclase associated protein [Gossypium hirsutum]

Seq. No. 398697
Seq. ID LIB3431-017-P1-N1-H9
Method BLASTN

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR (CAB) >gi_72749_pir_CDBH3 chlorophyll a/b-binding protein type III precursor - barley >gi_19023_emb_CAA44881 (X63197) type III LHCII CAB precursor protein [Hordeum vulgare]

```
Seq. No.      398708
Seq. ID      LIB3431-018-P1-K1-C12
Method       BLASTX
NCBI GI      g2501578
BLAST score   515
E value      3.0e-52
Match length  125
% identity    82
NCBI Description  ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047
                ethylene-responsive protein 1 - Para rubber tree
                >gi_1209317 (M88254) ethylene-inducible protein [Hevea
                brasiliensis]
```

```
Seq. No.      398709
Seq. ID       LIB3431-018-P1-K1-C4
Method        BLASTX
NCBI GI       g132105
BLAST score   739
E value       2.0e-78
Match length  137
% identity    99
NCBI Description  RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                (D00643) small subunit of ribulose-1,5-bisphosphate
                carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                carboxylase S [Oryza sativa]
```

```
Seq. No.      398710
Seq. ID      LIB3431-018-P1-K1-C6
Method       BLASTX
NCBI GI      g2497746
BLAST score   380
E value      2.0e-36
Match length  99
% identity    76
NCBI Description  NONSPECIFIC LIPID-TRANSFER PROTEIN 2 PRECURSOR (LTP 2)
                  >gi_951334 (U31766) lipid transfer protein precursor [Oryza
                  sativa]
```

```
Seq. No.          398711
Seq. ID           LIB3431-018-P1-K1-C7
Method            BLASTX
NCBI GI           g3789952
BLAST score       252
E value           2.0e-21
Match length      151
% identity        49
```


Seq. ID LIB3431-018-P1-K1-D7
 Method BLASTX
 NCBI GI g4803952
 BLAST score 461
 E value 8.0e-46
 Match length 115
 % identity 77
 NCBI Description (AC006202) hypothetical protein [Arabidopsis thaliana]

Seq. No. 398722
 Seq. ID LIB3431-018-P1-K1-E10
 Method BLASTX
 NCBI GI g125580
 BLAST score 791
 E value 2.0e-84
 Match length 181
 % identity 85
 NCBI Description PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_100839_pir_S15743 phosphoribulokinase (EC 2.7.1.19) - wheat >gi_5924030_emb_CAB56544.1_ (X51608) phosphoribulokinase [Triticum aestivum]

Seq. No. 398723
 Seq. ID LIB3431-018-P1-K1-E12
 Method BLASTX
 NCBI GI g671740
 BLAST score 342
 E value 4.0e-32
 Match length 63
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 398724
 Seq. ID LIB3431-018-P1-K1-E3
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 1.0e-19
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 398725
 Seq. ID LIB3431-018-P1-K1-E7
 Method BLASTN
 NCBI GI g2331140
 BLAST score 279
 E value 1.0e-155
 Match length 420
 % identity 97
 NCBI Description Oryza sativa water-stress inducible protein (WSI) mRNA, complete cds

Seq. No. 398726

Seq. ID LIB3431-018-P1-K1-E9
 Method BLASTX
 NCBI GI g320618
 BLAST score 746
 E value 2.0e-79
 Match length 159
 % identity 90
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 398727
 Seq. ID LIB3431-018-P1-K1-F10
 Method BLASTX
 NCBI GI g548605
 BLAST score 595
 E value 1.0e-61
 Match length 130
 % identity 91
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
 (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
 >gi_539055_pir_A48527 photosystem I protein psaK precursor
 - barley >gi_304220 (L12707) photosystem I PSI-K subunit
 [Hordeum vulgare]

Seq. No. 398728
 Seq. ID LIB3431-018-P1-K1-F11
 Method BLASTX
 NCBI GI g131388
 BLAST score 658
 E value 6.0e-69
 Match length 189
 % identity 72
 NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
 SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
 THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir_S16260
 photosystem II oxygen-evolving complex protein 1 - common
 wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408)
 33kDa oxygen evolving protein of photosystem II [Triticum
 aestivum]

Seq. No. 398729
 Seq. ID LIB3431-018-P1-K1-F12
 Method BLASTX
 NCBI GI g548605
 BLAST score 377
 E value 3.0e-36
 Match length 78
 % identity 95
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
 (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
 >gi_539055_pir_A48527 photosystem I protein psaK precursor
 - barley >gi_304220 (L12707) photosystem I PSI-K subunit
 [Hordeum vulgare]

Seq. No. 398730
 Seq. ID LIB3431-018-P1-K1-F8
 Method BLASTX
 NCBI GI g2570499
 BLAST score 191
 E value 1.0e-14
 Match length 38
 % identity 100
 NCBI Description (AF022732) 23kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 398731
 Seq. ID LIB3431-018-P1-K1-G10
 Method BLASTX
 NCBI GI g5305740
 BLAST score 759
 E value 8.0e-81
 Match length 186
 % identity 84
 NCBI Description (AF135862) precursor monofunctional aspartokinase [Glycine max]

Seq. No. 398732
 Seq. ID LIB3431-018-P1-K1-G11
 Method BLASTX
 NCBI GI g115787
 BLAST score 691
 E value 7.0e-73
 Match length 133
 % identity 99
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 398733
 Seq. ID LIB3431-018-P1-K1-G12
 Method BLASTX
 NCBI GI g5921185
 BLAST score 395
 E value 6.0e-47
 Match length 213
 % identity 50
 NCBI Description CYTOCHROME P450 76C1 >gi_2979548 (AC003680) putative 7-ethoxycoumarin O-deethylase [Arabidopsis thaliana]

Seq. No. 398734
 Seq. ID LIB3431-018-P1-K1-G2
 Method BLASTX
 NCBI GI g1173347
 BLAST score 932
 E value 1.0e-101
 Match length 185
 % identity 95
 NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)

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Seq. No.	398739
Seq. ID	LIB3431-018-P1-K1-G9
Method	BLASTX
NCBI GI	g3885888
BLAST score	326
E value	4.0e-30
Match length	89
% identity	76
NCBI Description	(AF093632) high mobility group protein [Oryza sativa]
Seq. No.	398740
Seq. ID	LIB3431-018-P1-K1-H10
Method	BLASTX
NCBI GI	g115793
BLAST score	869
E value	1.0e-93
Match length	192
% identity	85
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR (CAB) >gi_72749_pir_CDBH3 chlorophyll a/b-binding protein type III precursor - barley >gi_19023_emb_CAA44881_ (X63197) type III LHCII CAB precursor protein [Hordeum vulgare]
Seq. No.	398741
Seq. ID	LIB3431-018-P1-K1-H12
Method	BLASTX
NCBI GI	g710308
BLAST score	987
E value	1.0e-107
Match length	224
% identity	85
NCBI Description	(U11693) victorin binding protein [Avena sativa]
Seq. No.	398742
Seq. ID	LIB3431-018-P1-K1-H3
Method	BLASTX
NCBI GI	g113466
BLAST score	282
E value	8.0e-25
Match length	82
% identity	65
NCBI Description	ADP,ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT) >gi_72020_pir_XWNC ADP,ATP carrier protein - Neurospora crassa >gi_2977_emb_CAA25104_ (X00363) ADP/ATP carrier protein [Neurospora crassa]
Seq. No.	398743
Seq. ID	LIB3431-018-P1-K1-H4
Method	BLASTX
NCBI GI	g3126854
BLAST score	731
E value	2.0e-77
Match length	186
% identity	80
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

[illegible]

```
Seq. No.      398755
Seq. ID      LIB3431-018-P1-N1-B6
Method       BLASTX
NCBI GI      g115813
BLAST score   224
E value      3.0e-18
Match length  78
% identity    69
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                  CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
```

Seq. No.	398757
Seq. ID	LIB3431-018-P1-N1-B9
Method	BLASTN
NCBI GI	g11957
BLAST score	68
E value	4.0e-30
Match length	156
% identity	87
NCBI Description	Rice complete chloroplast genome

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Seq. No. 398759
 Seq. ID LIB3431-018-P1-N1-C4
 Method BLASTX
 NCBI GI g671740
 BLAST score 244
 E value 8.0e-21
 Match length 58
 % identity 79
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 398760
 Seq. ID LIB3431-018-P1-N1-C5
 Method BLASTX
 NCBI GI g548605
 BLAST score 338
 E value 9.0e-32
 Match length 73
 % identity 92
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
 >gi_539055_pir_A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No. 398761
 Seq. ID LIB3431-018-P1-N1-C6
 Method BLASTX
 NCBI GI g2407273
 BLAST score 268
 E value 1.0e-23
 Match length 53
 % identity 96
 NCBI Description (AF017359) lipid transfer protein LPT II [Oryza sativa]

Seq. No. 398762
 Seq. ID LIB3431-018-P1-N1-C8
 Method BLASTX
 NCBI GI g3980406
 BLAST score 313
 E value 8.0e-29
 Match length 93
 % identity 61
 NCBI Description (AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No. 398763
 Seq. ID LIB3431-018-P1-N1-D12
 Method BLASTX
 NCBI GI g115813
 BLAST score 267
 E value 3.0e-23
 Match length 83
 % identity 69
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330 (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

NCBI Description O.sativa mRNA for catalase

Seq. No. 398769
 Seq. ID LIB3431-018-P1-N1-E1
 Method BLASTX
 NCBI GI g3913641
 BLAST score 434
 E value 1.0e-60
 Match length 126
 % identity 96
 NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
 (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
 >gi_3041777_dbj_BAA25423_ (AB007194)
 fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No. 398770
 Seq. ID LIB3431-018-P1-N1-E10
 Method BLASTN
 NCBI GI g21838
 BLAST score 67
 E value 3.0e-29
 Match length 204
 % identity 85
 NCBI Description T.aestivum PRK gene for ribulose-5-phosphate kinase

Seq. No. 398771
 Seq. ID LIB3431-018-P1-N1-E11
 Method BLASTX
 NCBI GI g2864617
 BLAST score 200
 E value 2.0e-15
 Match length 85
 % identity 53
 NCBI Description (AL021811) H+-transporting ATP synthase chain9 - like
 protein [Arabidopsis thaliana] >gi_5730141_emb_CAB52473.1_
 (AJ245574) ATP synthase beta chain precursor (subunit II)
 [Arabidopsis thaliana]

Seq. No. 398772
 Seq. ID LIB3431-018-P1-N1-E12
 Method BLASTX
 NCBI GI g671740
 BLAST score 284
 E value 3.0e-25
 Match length 63
 % identity 84
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
 construct]

Seq. No. 398773
 Seq. ID LIB3431-018-P1-N1-E2
 Method BLASTX
 NCBI GI g2407279
 BLAST score 279
 E value 4.0e-42
 Match length 94
 % identity 93


```
Seq. No.      398779
Seq. ID       LIB3431-018-P1-N1-F10
Method        BLASTX
NCBI GI       g548605
BLAST score   368
E value       3.0e-35
Match length  76
% identity    95
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                >gi_539055_pir_A48527 photosystem I protein psaK precursor
                - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                [Hordeum vulgare]
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Seq. No.      398780
Seq. ID      LIB3431-018-P1-N1-F11
Method       BLASTX
NCBI GI      g482311
BLAST score   297
E value      3.0e-41
Match length  91
% identity    99
NCBI Description  photosystem II oxygen-evolving complex protein 1 - rice
                  (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
```

```
Seq. No.      398781
Seq. ID      LIB3431-018-P1-N1-F5
Method       BLASTN
NCBI GI      g20369
BLAST score   382
E value      0.0e+00
Match length  382
% identity    100
NCBI Description  Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
synthetase (EC 6.3.1.2) (clone lambda-GS31)
>gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of
chloroplast localising glutamine synthetase
```

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Seq. No.          398782
Seq. ID           LIB3431-018-P1-N1-F7
Method            BLASTX
NCBI GI           g1477428
BLAST score       294
E value           2.0e-26
Match length      59
% identity        97
NCBI Description   (X99623) alpha-tubulin 1 [Hordeum vulgare]
```

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Seq. No.          398783
Seq. ID           LIB3431-018-P1-N1-F8
Method            BLASTX
NCBI GI           g4079798
BLAST score       298
E value           8.0e-43
Match length      93
% identity        88
```


Seq. No. 398789
 Seq. ID LIB3431-018-P1-N1-G9
 Method BLASTN
 NCBI GI g3885887
 BLAST score 365
 E value 0.0e+00
 Match length 365
 % identity 100
 NCBI Description Oryza sativa high mobility group protein (HMG) mRNA, complete cds

Seq. No. 398790
 Seq. ID LIB3431-018-P1-N1-H10
 Method BLASTX
 NCBI GI g115794
 BLAST score 542
 E value 2.0e-55
 Match length 114
 % identity 90
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE III CAB-13) >gi_72748_pir_CDT033 chlorophyll a/b-binding protein type III precursor (cab-13) - tomato >gi_19277_emb_CAA42818_(X60275) LHCII type III [Lycopersicon esculentum]

Seq. No. 398791
 Seq. ID LIB3431-018-P1-N1-H12
 Method BLASTN
 NCBI GI g710307
 BLAST score 36
 E value 1.0e-10
 Match length 52
 % identity 92
 NCBI Description Avena sativa victorin binding protein mRNA, complete cds

Seq. No. 398792
 Seq. ID LIB3431-018-P1-N1-H2
 Method BLASTX
 NCBI GI g3881189
 BLAST score 146
 E value 2.0e-15
 Match length 93
 % identity 43
 NCBI Description (Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL:C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST y

Seq. No. 398793
 Seq. ID LIB3431-018-P1-N1-H4
 Method BLASTX
 NCBI GI g115802
 BLAST score 195
 E value 5.0e-15
 Match length 40
 % identity 90

% identity 100
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 398799
 Seq. ID LIB3431-019-P1-K1-A11
 Method BLASTX
 NCBI GI g1085987
 BLAST score 231
 E value 2.0e-19
 Match length 45
 % identity 98
 NCBI Description light harvesting chlorophyll a protein precursor - Norway spruce >gi_607148_emb_CAA57407_ (X81808) light harvesting chlorophyll a /b-binding protein Lhcb1*1 [Picea abies]

Seq. No. 398800
 Seq. ID LIB3431-019-P1-K1-A12
 Method BLASTN
 NCBI GI g4761113
 BLAST score 47
 E value 3.0e-17
 Match length 51
 % identity 98
 NCBI Description Allium grayi 5S ribosomal RNA gene, complete sequence

Seq. No. 398801
 Seq. ID LIB3431-019-P1-K1-A4
 Method BLASTX
 NCBI GI g3789954
 BLAST score 691
 E value 4.0e-73
 Match length 127
 % identity 100
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 398802
 Seq. ID LIB3431-019-P1-K1-A5
 Method BLASTX
 NCBI GI g126894
 BLAST score 535
 E value 1.0e-54
 Match length 137
 % identity 78
 NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
 >gi_319832_pir_DEPUGW malate dehydrogenase (EC 1.1.1.37) precursor, glyoxysomal - watermelon >gi_167284 (M33148) glyoxysomal malate dehydrogenase precursor (EC 1.1.1.37) [Citrullus vulgaris]

Seq. No. 398803
 Seq. ID LIB3431-019-P1-K1-A6
 Method BLASTX
 NCBI GI g5442410
 BLAST score 390
 E value 1.0e-37

Match length 137
 % identity 57
 NCBI Description (AF159254) ascorbate peroxidase [Zantedeschia aethiopica]

Seq. No. 398804
 Seq. ID LIB3431-019-P1-K1-A7
 Method BLASTX
 NCBI GI g320618
 BLAST score 689
 E value 9.0e-73
 Match length 150
 % identity 87
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 398805
 Seq. ID LIB3431-019-P1-K1-A9
 Method BLASTX
 NCBI GI g2982453
 BLAST score 149
 E value 9.0e-15
 Match length 77
 % identity 58
 NCBI Description (AL022223) fructose-bisphosphate aldolase-like protein
 [Arabidopsis thaliana]

Seq. No. 398806
 Seq. ID LIB3431-019-P1-K1-B1
 Method BLASTX
 NCBI GI g2809245
 BLAST score 298
 E value 6.0e-27
 Match length 78
 % identity 72
 NCBI Description (AC002560) F21B7.14 [Arabidopsis thaliana]

Seq. No. 398807
 Seq. ID LIB3431-019-P1-K1-B11
 Method BLASTX
 NCBI GI g4038594
 BLAST score 280
 E value 8.0e-25
 Match length 84
 % identity 62
 NCBI Description (AJ222798) tDET1 protein [Lycopersicon esculentum]
 >gi_4454332_emb_CAA11914_ (AJ224356) tDET1 protein
 [Lycopersicon esculentum]

Seq. No. 398808
 Seq. ID LIB3431-019-P1-K1-B12
 Method BLASTX
 NCBI GI g3885882
 BLAST score 390
 E value 7.0e-38

09584015-101000

Seq. No. 398818
Seq. ID LIB3431-019-P1-K1-C4
Method BLASTX
NCBI GI g3913018
BLAST score 712
E value 2.0e-75
Match length 136
% identity 99
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
(ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic
aldolase [Oryza sativa]

Seq. No. 398819
Seq. ID LIB3431-019-P1-K1-C5
Method BLASTX
NCBI GI g3776005
BLAST score 372
E value 1.0e-35
Match length 76
% identity 95
NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No. 398820
Seq. ID LIB3431-019-P1-K1-C6
Method BLASTX
NCBI GI g3776005
BLAST score 287
E value 1.0e-25
Match length 76
% identity 78
NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No. 398821
Seq. ID LIB3431-019-P1-K1-C7
Method BLASTX
NCBI GI g1173347
BLAST score 473
E value 2.0e-47
Match length 107
% identity 89
NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
>gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC
3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
(X65540) sedoheptulose-1,7-bisphosphatase [Triticum
aestivum]

Seq. No. 398822
Seq. ID LIB3431-019-P1-K1-C8
Method BLASTX
NCBI GI g132105
BLAST score 538
E value 4.0e-55
Match length 120
% identity 85
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9

E value 5.0e-66
 Match length 139
 % identity 91
 NCBI Description UROPORPHYRINOGEN DECARBOXYLASE (UPD)
 >gi_1362169_pir_S55733 uroporphyrinogen decarboxylase -
 barley >gi_1016347_emb_CAA58039_ (X82832) uroporphyrinogen
 decarboxylase [Hordeum vulgare]

Seq. No. 398828
 Seq. ID LIB3431-019-P1-K1-D4
 Method BLASTN
 NCBI GI g6015437
 BLAST score 38
 E value 7.0e-12
 Match length 38
 % identity 100
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 398829
 Seq. ID LIB3431-019-P1-K1-D5
 Method BLASTN
 NCBI GI g3821780
 BLAST score 36
 E value 1.0e-10
 Match length 47
 % identity 66
 NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 398830
 Seq. ID LIB3431-019-P1-K1-D7
 Method BLASTX
 NCBI GI g115787
 BLAST score 508
 E value 1.0e-51
 Match length 117
 % identity 87
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
 protein 2R precursor - rice >gi_20182_emb_CAA32109
 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
 [Oryza sativa]

Seq. No. 398831
 Seq. ID LIB3431-019-P1-K1-D8
 Method BLASTX
 NCBI GI g132105
 BLAST score 609
 E value 2.0e-63
 Match length 131
 % identity 88
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

09634016 101000

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Seq. No.          398846
Seq. ID           LIB3431-019-P1-K1-F4
Method            BLASTX
NCBI GI           g82080
BLAST score       336
E value           2.0e-31
Match length      95
```


E value 3.0e-42
 Match length 95
 % identity 95
 NCBI Description (AF093629) inorganic pyrophosphatase [*Oryza sativa*]

Seq. No. 398862
 Seq. ID LIB3431-019-P1-K1-H6
 Method BLASTX
 NCBI GI g2795806
 BLAST score 498
 E value 2.0e-50
 Match length 141
 % identity 70
 NCBI Description (AC003674) unknown protein [*Arabidopsis thaliana*]

Seq. No. 398863
 Seq. ID LIB3431-019-P1-K1-H7
 Method BLASTX
 NCBI GI g1164988
 BLAST score 345
 E value 2.0e-32
 Match length 124
 % identity 55
 NCBI Description (X94335) YOR3513c [*Saccharomyces cerevisiae*]

Seq. No. 398864
 Seq. ID LIB3431-019-P1-K1-H9
 Method BLASTX
 NCBI GI g266893
 BLAST score 661
 E value 1.0e-69
 Match length 130
 % identity 95
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
 CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
 >gi_322416_pir_S28172 ribulose-bisphosphate carboxylase
 activase - cucumber >gi_18284_emb_CAA47906_ (X67674)
 rubisco activase [*Cucumis sativus*]

Seq. No. 398865
 Seq. ID LIB3431-019-P1-N1-A10
 Method BLASTN
 NCBI GI g2072554
 BLAST score 233
 E value 1.0e-128
 Match length 237
 % identity 100
 NCBI Description *Oryza sativa* metallothionein-like protein mRNA, complete
 cds

Seq. No. 398866
 Seq. ID LIB3431-019-P1-N1-A11
 Method BLASTX
 NCBI GI g1085987
 BLAST score 231
 E value 2.0e-19
 Match length 45

05634015-101000

% identity 98
NCBI Description light harvesting chlorophyll a protein precursor - Norway spruce >gi_607148_emb_CAA57407_ (X81808) light harvesting chlorophyll a /b-binding protein Lhcb1*1 [Picea abies]

Seq. No. 398867
Seq. ID LIB3431-019-P1-N1-A2
Method BLASTN
NCBI GI g218207
BLAST score 161
E value 2.0e-85
Match length 245
% identity 91
NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No. 398868
Seq. ID LIB3431-019-P1-N1-A4
Method BLASTX
NCBI GI g3789954
BLAST score 390
E value 1.0e-37
Match length 72
% identity 100
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 398869
Seq. ID LIB3431-019-P1-N1-A6
Method BLASTX
NCBI GI g5442410
BLAST score 179
E value 5.0e-13
Match length 78
% identity 49
NCBI Description (AF159254) ascorbate peroxidase [Zantedeschia aethiopica]

Seq. No. 398870
Seq. ID LIB3431-019-P1-N1-A7
Method BLASTX
NCBI GI g115787
BLAST score 409
E value 6.0e-40
Match length 77
% identity 100
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 398871
Seq. ID LIB3431-019-P1-N1-A9
Method BLASTX
NCBI GI g2191138
BLAST score 287

E value 1.0e-25
 Match length 64
 % identity 83
 NCBI Description (AF007269) A_IG002N01.18 gene product [Arabidopsis thaliana]

Seq. No. 398872
 Seq. ID LIB3431-019-P1-N1-B1
 Method BLASTX
 NCBI GI g2809245
 BLAST score 283
 E value 3.0e-25
 Match length 64
 % identity 83
 NCBI Description (AC002560) F21B7.14 [Arabidopsis thaliana]

Seq. No. 398873
 Seq. ID LIB3431-019-P1-N1-B11
 Method BLASTX
 NCBI GI g4038594
 BLAST score 233
 E value 2.0e-19
 Match length 67
 % identity 63
 NCBI Description (AJ222798) tDET1 protein [Lycopersicon esculentum]
 >gi_4454332_emb_CAA11914_ (AJ224356) tDET1 protein [Lycopersicon esculentum]

Seq. No. 398874
 Seq. ID LIB3431-019-P1-N1-B12
 Method BLASTN
 NCBI GI g3885881
 BLAST score 345
 E value 0.0e+00
 Match length 373
 % identity 98
 NCBI Description Oryza sativa inorganic pyrophosphatase (IPP) mRNA, complete cds

Seq. No. 398875
 Seq. ID LIB3431-019-P1-N1-B4
 Method BLASTX
 NCBI GI g115813
 BLAST score 176
 E value 1.0e-12
 Match length 41
 % identity 80
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 398876
 Seq. ID LIB3431-019-P1-N1-B6
 Method BLASTX
 NCBI GI g461753
 BLAST score 406
 E value 1.0e-39

OE17 protein [Pisum sativum]

Seq. No. 398887
 Seq. ID LIB3431-019-P1-N1-D3
 Method BLASTX
 NCBI GI g6014938
 BLAST score 173
 E value 2.0e-12
 Match length 34
 % identity 94
 NCBI Description UROPORPHYRINOGEN DECARBOXYLASE PRECURSOR (UPD) >gi_3420233
 (AF058763) uroporphyrinogen decarboxylase [Zea mays]

Seq. No. 398888
 Seq. ID LIB3431-019-P1-N1-D7
 Method BLASTX
 NCBI GI g421916
 BLAST score 162
 E value 4.0e-11
 Match length 29
 % identity 100
 NCBI Description chlorophyll a/b-binding protein - English ivy (fragment)
 >gi_12582_emb_CAA48410_ (X68333) light harvesting
 chlorophyll a /b binding protein [Hedera helix]

Seq. No. 398889
 Seq. ID LIB3431-019-P1-N1-D8
 Method BLASTX
 NCBI GI g347451
 BLAST score 387
 E value 2.0e-37
 Match length 72
 % identity 97
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
 sativa].

Seq. No. 398890
 Seq. ID LIB3431-019-P1-N1-D9
 Method BLASTX
 NCBI GI g3036951
 BLAST score 310
 E value 2.0e-28
 Match length 61
 % identity 98
 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein
 [Nicotiana sylvestris]

Seq. No. 398891
 Seq. ID LIB3431-019-P1-N1-E4
 Method BLASTX
 NCBI GI g5764049
 BLAST score 252
 E value 2.0e-21
 Match length 67
 % identity 70
 NCBI Description (Y16832) alpha-1,3-mannosyl-glycoprotein
 beta-1,2-N-acetylglucosaminyltransferase [Nicotiana

tabacum]

Seq. No. 398892
 Seq. ID LIB3431-019-P1-N1-E6
 Method BLASTN
 NCBI GI g2331130
 BLAST score 189
 E value 1.0e-102
 Match length 193
 % identity 99
 NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds

Seq. No. 398893
 Seq. ID LIB3431-019-P1-N1-F10
 Method BLASTN
 NCBI GI g3075487
 BLAST score 240
 E value 1.0e-132
 Match length 260
 % identity 98
 NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No. 398894
 Seq. ID LIB3431-019-P1-N1-F2
 Method BLASTX
 NCBI GI g1777961
 BLAST score 194
 E value 1.0e-14
 Match length 73
 % identity 58
 NCBI Description (U56406) methyljasmonate-inducible lipoxygenase 2 [Hordeum vulgare]

Seq. No. 398895
 Seq. ID LIB3431-019-P1-N1-F4
 Method BLASTX
 NCBI GI g115813
 BLAST score 243
 E value 1.0e-20
 Match length 55
 % identity 85
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_(X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 398896
 Seq. ID LIB3431-019-P1-N1-F6
 Method BLASTX
 NCBI GI g710308
 BLAST score 147
 E value 2.0e-09
 Match length 27
 % identity 96
 NCBI Description (U11693) victorin binding protein [Avena sativa]

Seq. No. 398897
 Seq. ID LIB3431-019-P1-N1-F7
 Method BLASTX
 NCBI GI g3126854
 BLAST score 345
 E value 1.0e-32
 Match length 65
 % identity 100
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 398898
 Seq. ID LIB3431-019-P1-N1-F8
 Method BLASTN
 NCBI GI g1835730
 BLAST score 219
 E value 1.0e-120
 Match length 255
 % identity 96
 NCBI Description Oryza sativa photosystem II 10 kDa polypeptide mRNA, complete cds

Seq. No. 398899
 Seq. ID LIB3431-019-P1-N1-F9
 Method BLASTN
 NCBI GI g3075487
 BLAST score 338
 E value 0.0e+00
 Match length 338
 % identity 100
 NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No. 398900
 Seq. ID LIB3431-019-P1-N1-G1
 Method BLASTX
 NCBI GI g1321627
 BLAST score 231
 E value 3.0e-19
 Match length 55
 % identity 82
 NCBI Description (D83656) thylakoid-bound ascorbate peroxidase [Cucurbita sp.]

Seq. No. 398901
 Seq. ID LIB3431-019-P1-N1-G10
 Method BLASTX
 NCBI GI g289920
 BLAST score 286
 E value 1.0e-25
 Match length 58
 % identity 95
 NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No. 398902
 Seq. ID LIB3431-019-P1-N1-G2
 Method BLASTX

NCBI GI g120661
 BLAST score 251
 E value 2.0e-21
 Match length 50
 % identity 92
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST
 PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate
 dehydrogenase A-subunit precursor [Nicotiana tabacum]

Seq. No. 398903
 Seq. ID LIB3431-019-P1-N1-G5
 Method BLASTN
 NCBI GI g218171
 BLAST score 215
 E value 1.0e-117
 Match length 243
 % identity 97
 NCBI Description Oryza sativa mRNA for type I light-harvesting chlorophyll
 a/b binding protein of photosystem II (LHCPII), complete
 cds

Seq. No. 398904
 Seq. ID LIB3431-019-P1-N1-G6
 Method BLASTX
 NCBI GI g1652203
 BLAST score 153
 E value 5.0e-10
 Match length 78
 % identity 38
 NCBI Description (D90903) hypothetical protein [Synechocystis sp.]

Seq. No. 398905
 Seq. ID LIB3431-019-P1-N1-G7
 Method BLASTX
 NCBI GI g132105
 BLAST score 310
 E value 1.0e-30
 Match length 68
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 398906
 Seq. ID LIB3431-019-P1-N1-H11
 Method BLASTX
 NCBI GI g3789954
 BLAST score 184
 E value 9.0e-14
 Match length 33
 % identity 97

[illegible]

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Seq. No.      398916
Seq. ID      LIB3431-020-P1-K1-B12
Method       BLASTX
NCBI GI      g121446
BLAST score  160
```


Match length 90
 % identity 58
 NCBI Description (AC002561) unknown protein [Arabidopsis thaliana]

Seq. No. 398922
 Seq. ID LIB3431-020-P1-K1-B9
 Method BLASTX
 NCBI GI g132105
 BLAST score 391
 E value 7.0e-38
 Match length 124
 % identity 64
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 398923
 Seq. ID LIB3431-020-P1-K1-C1
 Method BLASTX
 NCBI GI g170404
 BLAST score 565
 E value 3.0e-68
 Match length 137
 % identity 96
 NCBI Description (M14444) chlorophyll a/b-binding protein Cab-3C [Lycopersicon esculentum]

Seq. No. 398924
 Seq. ID LIB3431-020-P1-K1-C10
 Method BLASTX
 NCBI GI g1346874
 BLAST score 152
 E value 8.0e-10
 Match length 49
 % identity 61
 NCBI Description PHOTOSYSTEM II REACTION CENTER W PROTEIN >gi_1016177 (U30821) subunit of the water oxidation complex on the luminal surface of the photosystem II reaction center complex [Cyanophora paradoxa]

Seq. No. 398925
 Seq. ID LIB3431-020-P1-K1-C11
 Method BLASTX
 NCBI GI g3126854
 BLAST score 646
 E value 1.0e-67
 Match length 140
 % identity 89
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 398926


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NCBI GI      g3915131
BLAST score   582
E value      3.0e-60
Match length 112
% identity   100
NCBI Description THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1)
>gi_426442_dbj_BAA04864_ (D21836) thioredoxin h [Oryza
sativa] >gi_454882_dbj_BAA05546_ (D26547) rice thioredoxin
h [Oryza sativa] >gi_1930072 (U92541) thioredoxin h [Oryza
sativa]

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Seq. No.      398932
Seq. ID      LIB3431-020-P1-K1-D4
Method       BLASTX
NCBI GI      g2570511
BLAST score   662
E value      1.0e-69
Match length  127
% identity    98
NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]
```

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Seq. No.      398933
Seq. ID      LIB3431-020-P1-K1-D5
Method       BLASTX
NCBI GI      g3047117
BLAST score   740
E value      1.0e-78
Match length  144
% identity    97
NCBI Description (AF058919) similar to ATP-dependent RNA helicases
               [Arabidopsis thaliana]
```

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Seq. No.          398934
Seq. ID           LIB3431-020-P1-K1-D7
Method            BLASTX
NCBI GI           g1617206
BLAST score       180
E value           3.0e-13
Match length      49
% identity        71
NCBI Description   (Z72489) CP12 [Pisum sativum]
```

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Seq. No.      398935
Seq. ID      LIB3431-020-P1-K1-D8
Method       BLASTX
NCBI GI      g320618
BLAST score   632
E value      5.0e-66
Match length  137
% identity    88
NCBI Description  chlorophyll a/b-binding protein I precursor - rice
>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
>gi_227611_prf_1707316A chlorophyll a/b binding protein 1
[Oryza sativa]
```

Seq. No. 398936

Seq. ID	LIB3431-020-P1-K1-D9
Method	BLASTX
NCBI GI	g2582822
BLAST score	458
E value	1.0e-45
Match length	108
% identity	80
NCBI Description	(Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]
Seq. No.	398937
Seq. ID	LIB3431-020-P1-K1-E1
Method	BLASTX
NCBI GI	g4886307
BLAST score	543
E value	1.0e-55
Match length	123
% identity	87
NCBI Description	(AJ242588) 1-deoxy-d-xylulose-5-phosphate reductoisomerase [Arabidopsis thaliana]
Seq. No.	398938
Seq. ID	LIB3431-020-P1-K1-E10
Method	BLASTX
NCBI GI	g2570515
BLAST score	219
E value	1.0e-17
Match length	47
% identity	91
NCBI Description	(AF022740) glycolate oxidase [Oryza sativa]
Seq. No.	398939
Seq. ID	LIB3431-020-P1-K1-E11
Method	BLASTX
NCBI GI	g320618
BLAST score	607
E value	4.0e-63
Match length	133
% identity	87
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf_1707316A chlorophyll a/b binding protein 1 [Oryza sativa]
Seq. No.	398940
Seq. ID	LIB3431-020-P1-K1-E12
Method	BLASTX
NCBI GI	g132105
BLAST score	759
E value	6.0e-81
Match length	139
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose biphosphate
 carboxylase S [Oryza sativa]

Seq. No. 398941
 Seq. ID LIB3431-020-P1-K1-E2
 Method BLASTX
 NCBI GI g3345477
 BLAST score 491
 E value 2.0e-49
 Match length 140
 % identity 69
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 398942
 Seq. ID LIB3431-020-P1-K1-E3
 Method BLASTN
 NCBI GI g6015437
 BLAST score 35
 E value 6.0e-10
 Match length 35
 % identity 100
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 398943
 Seq. ID LIB3431-020-P1-K1-E5
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 1.0e-19
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 398944
 Seq. ID LIB3431-020-P1-K1-E6
 Method BLASTX
 NCBI GI g115787
 BLAST score 417
 E value 7.0e-41
 Match length 121
 % identity 74
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
 protein 2R precursor - rice >gi_20182_emb_CAA32109
 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
 [Oryza sativa]

Seq. No. 398945
 Seq. ID LIB3431-020-P1-K1-E7
 Method BLASTX
 NCBI GI g1835731
 BLAST score 559

00684016-101000

E value 2.0e-57
Match length 106
% identity 100
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 398946
Seq. ID LIB3431-020-P1-K1-E8
Method BLASTX
NCBI GI g2407281
BLAST score 625
E value 3.0e-65
Match length 117
% identity 99
NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 398947
Seq. ID LIB3431-020-P1-K1-E9
Method BLASTX
NCBI GI g2565305
BLAST score 605
E value 5.0e-63
Match length 119
% identity 96
NCBI Description (AF024589) glycine decarboxylase P subunit [Hordeum sp. x Triticum sp.]

Seq. No. 398948
Seq. ID LIB3431-020-P1-K1-F1
Method BLASTN
NCBI GI g3789951
BLAST score 188
E value 1.0e-101
Match length 380
% identity 96
NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 398949
Seq. ID LIB3431-020-P1-K1-F11
Method BLASTX
NCBI GI g1661160
BLAST score 523
E value 3.0e-53
Match length 115
% identity 85
NCBI Description (U74295) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 398950
Seq. ID LIB3431-020-P1-K1-F12
Method BLASTX
NCBI GI g728744
BLAST score 338
E value 1.0e-54
Match length 152
% identity 76

NCBI Description AUXIN-INDUCED PROTEIN PCNT115 >gi_100305_pir__S16390
auxin-induced protein - common tobacco
>gi_19799_emb_CAA39708_ (X56267) auxin-induced protein
[Nicotiana tabacum]

Seq. No. 398951
Seq. ID LIB3431-020-P1-K1-F2
Method BLASTX
NCBI GI g3789952
BLAST score 788
E value 2.0e-84
Match length 152
% identity 96
NCBI Description (AF094775) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 398952
Seq. ID LIB3431-020-P1-K1-F3
Method BLASTX
NCBI GI g115772
BLAST score 211
E value 2.0e-17
Match length 57
% identity 77
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi_82460_pir_S03705 chlorophyll a/b-binding protein 1R precursor - rice >gi_20178_emb_CAA32108 (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235) [Oryza sativa]

Seq. No. 398953
Seq. ID LIB3431-020-P1-K1-F4
Method BLASTX
NCBI GI g6002055
BLAST score 634
E value 3.0e-66
Match length 151
% identity 77
NCBI Description (AJ249794) lipoxygenase [Arabidopsis thaliana]

Seq. No. 398954
Seq. ID LIB3431-020-P1-K1-F8
Method BLASTX
NCBI GI g3345477
BLAST score 316
E value 5.0e-29
Match length 59
% identity 100
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 398955
Seq. ID LIB3431-020-P1-K1-F9
Method BLASTX
NCBI GI g131225
BLAST score 570
E value 7.0e-59
Match length 119

% identity 93
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 398956
 Seq. ID LIB3431-020-P1-K1-G10
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 398957
 Seq. ID LIB3431-020-P1-K1-G11
 Method BLASTX
 NCBI GI g2462763
 BLAST score 322
 E value 2.0e-44
 Match length 124
 % identity 79
 NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 398958
 Seq. ID LIB3431-020-P1-K1-G12
 Method BLASTX
 NCBI GI g871931
 BLAST score 490
 E value 2.0e-49
 Match length 125
 % identity 80
 NCBI Description (D30763) ferredoxin [Oryza sativa]

Seq. No. 398959
 Seq. ID LIB3431-020-P1-K1-G6
 Method BLASTN
 NCBI GI g5670155
 BLAST score 43
 E value 4.0e-15
 Match length 75
 % identity 89
 NCBI Description Oryza sativa subsp. japonica BAC clone 34K24, complete sequence

Seq. No. 398960
 Seq. ID LIB3431-020-P1-K1-G7
 Method BLASTN
 NCBI GI g21810
 BLAST score 38
 E value 9.0e-12
 Match length 38

ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 398965
Seq. ID LIB3431-020-P1-K1-H3
Method BLASTX
NCBI GI g4583546
BLAST score 145
E value 6.0e-09
Match length 70
% identity 40
NCBI Description (AJ010819) GrpE protein [Arabidopsis thaliana]

Seq. No. 398966
Seq. ID LIB3431-020-P1-K1-H4
Method BLASTX
NCBI GI g2270994
BLAST score 231
E value 4.0e-19
Match length 125
% identity 42
NCBI Description (AF004809) Ca+2-binding EF hand protein [Glycine max]

Seq. No. 398967
Seq. ID LIB3431-020-P1-K1-H5
Method BLASTX
NCBI GI g4097587
BLAST score 250
E value 3.0e-21
Match length 69
% identity 72
NCBI Description (U64926) NTGP5 [Nicotiana tabacum]

Seq. No. 398968
Seq. ID LIB3431-020-P1-K1-H7
Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 9.0e-20
Match length 44
% identity 100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 398969
Seq. ID LIB3431-020-P1-N1-A2
Method BLASTN
NCBI GI g3342030
BLAST score 85
E value 7.0e-40
Match length 109
% identity 94
NCBI Description Joinvillea ascendens 18S small subunit ribosomal RNA gene, complete sequence

09584015-101000

Method BLASTX
 NCBI GI g1346875
 BLAST score 251
 E value 2.0e-21
 Match length 79
 % identity 57
 NCBI Description PHOTOSYSTEM II REACTION CENTER W PROTEIN
 >gi_1185169_emb_CAA91652_ (Z67753) PSII, protein W, 13 kDa
 [Odontella sinensis]

Seq. No. 398976
 Seq. ID LIB3431-020-P1-N1-C2
 Method BLASTN
 NCBI GI g20181
 BLAST score 63
 E value 6.0e-27
 Match length 91
 % identity 92
 NCBI Description Rice cab2R gene for light harvesting chlorophyll
 a/b-binding protein

Seq. No. 398977
 Seq. ID LIB3431-020-P1-N1-C4
 Method BLASTN
 NCBI GI g3789951
 BLAST score 223
 E value 1.0e-122
 Match length 358
 % identity 90
 NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor
 (Cab27) mRNA, nuclear gene encoding chloroplast protein,
 complete cds

Seq. No. 398978
 Seq. ID LIB3431-020-P1-N1-C8
 Method BLASTN
 NCBI GI g2072554
 BLAST score 269
 E value 1.0e-149
 Match length 357
 % identity 94
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
 cds

Seq. No. 398979
 Seq. ID LIB3431-020-P1-N1-C9
 Method BLASTN
 NCBI GI g1519250
 BLAST score 212
 E value 1.0e-115
 Match length 323
 % identity 91
 NCBI Description Oryza sativa GF14-c protein mRNA, complete cds

Seq. No. 398980
 Seq. ID LIB3431-020-P1-N1-D11
 Method BLASTX

Seq. No. 399000
 Seq. ID LIB3431-020-P1-N1-F6
 Method BLASTX
 NCBI GI g4079798
 BLAST score 153
 E value 3.0e-10
 Match length 32
 % identity 94
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 399001
 Seq. ID LIB3431-020-P1-N1-F7
 Method BLASTX
 NCBI GI g710308
 BLAST score 381
 E value 1.0e-36
 Match length 79
 % identity 86
 NCBI Description (U11693) victorin binding protein [Avena sativa]

Seq. No. 399002
 Seq. ID LIB3431-020-P1-N1-F9
 Method BLASTX
 NCBI GI g3345477
 BLAST score 204
 E value 7.0e-16
 Match length 46
 % identity 80
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 399003
 Seq. ID LIB3431-020-P1-N1-G10
 Method BLASTX
 NCBI GI g2462750
 BLAST score 269
 E value 1.0e-23
 Match length 71
 % identity 70
 NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 399004
 Seq. ID LIB3431-020-P1-N1-G11
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 1.0e-19
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 399005
 Seq. ID LIB3431-020-P1-N1-G12

Method BLASTX
 NCBI GI g482311
 BLAST score 571
 E value 4.0e-59
 Match length 115
 % identity 97
 NCBI Description photosystem II oxygen-evolving complex protein 1 - rice
 (strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving
 complex protein 1 [Oryza sativa]

Seq. No. 399050
 Seq. ID LIB3431-021-P1-K1-D7
 Method BLASTX
 NCBI GI g1346109
 BLAST score 318
 E value 3.0e-29
 Match length 59
 % identity 100
 NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
 PROTEIN (GPB-LR) (RWD) >gi_540535_dbj_BAA07404_ (D38231)
 RWD [Oryza sativa]

Seq. No. 399051
 Seq. ID LIB3431-021-P1-K1-D8
 Method BLASTX
 NCBI GI g131225
 BLAST score 578
 E value 1.0e-59
 Match length 124
 % identity 90
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
 V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein
 precursor - barley >gi_167087 (M61146) photosystem I
 hydrophobic protein [Hordeum vulgare]

Seq. No. 399052
 Seq. ID LIB3431-021-P1-K1-D9
 Method BLASTX
 NCBI GI g4467099
 BLAST score 482
 E value 2.0e-48
 Match length 119
 % identity 85
 NCBI Description (AL035538) glycine hydroxymethyltransferase like protein
 [Arabidopsis thaliana]

Seq. No. 399053
 Seq. ID LIB3431-021-P1-K1-E1
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

09584015-101000

% identity 100
NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 399070
Seq. ID LIB3431-021-P1-K1-G1
Method BLASTN
NCBI GI g304219
BLAST score 53
E value 6.0e-21
Match length 129
% identity 85
NCBI Description Hordeum vulgare chloroplast photosystem I PSK-I subunit mRNA, complete cds

Seq. No. 399071
Seq. ID LIB3431-021-P1-K1-G10
Method BLASTN
NCBI GI g20262
BLAST score 95
E value 9.0e-46
Match length 190
% identity 88
NCBI Description O.sativa light-induced mRNA

Seq. No. 399072
Seq. ID LIB3431-021-P1-K1-G12
Method BLASTX
NCBI GI g548605
BLAST score 489
E value 2.0e-54
Match length 131
% identity 81
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
>gi_539055_pir_A48527 photosystem I protein psaK precursor
- barley >gi_304220 (L12707) photosystem I PSI-K subunit
[Hordeum vulgare]

Seq. No. 399073
Seq. ID LIB3431-021-P1-K1-G2
Method BLASTN
NCBI GI g6015437
BLAST score 35
E value 6.0e-10
Match length 35
% identity 100
NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 399074
Seq. ID LIB3431-021-P1-K1-G3
Method BLASTX
NCBI GI g3800878
BLAST score 543
E value 1.0e-55
Match length 150
% identity 71
NCBI Description (AF096281) threonine dehydratase/deaminase [Arabidopsis

10

09684016-101000

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09684016-101000

000T0T"9T08960

% identity 82
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 399113
Seq. ID LIB3431-021-P1-N1-D9
Method BLASTN
NCBI GI g438246
BLAST score 56
E value 1.0e-22
Match length 92
% identity 90
NCBI Description S.tuberosum mRNA for glycine hydroxymethyltransferase

Seq. No. 399114
Seq. ID LIB3431-021-P1-N1-E10
Method BLASTN
NCBI GI g1835730
BLAST score 144
E value 2.0e-75
Match length 156
% identity 98
NCBI Description Oryza sativa photosystem II 10 kDa polypeptide mRNA, complete cds

Seq. No. 399115
Seq. ID LIB3431-021-P1-N1-E11
Method BLASTX
NCBI GI g2072555
BLAST score 233
E value 3.0e-19
Match length 44
% identity 98
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 399116
Seq. ID LIB3431-021-P1-N1-E12
Method BLASTX
NCBI GI g3738261
BLAST score 368
E value 4.0e-35
Match length 83
% identity 92
NCBI Description (AB018412) chloroplast phosphoglycerate kinase [Populus nigra]

Seq. No. 399117
Seq. ID LIB3431-021-P1-N1-E4
Method BLASTX
NCBI GI g1835731
BLAST score 252
E value 1.0e-21
Match length 65

DocId:34016116

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Seq. No.      399144
Seq. ID      HIB3431-022-P1-K1-A7
Method       BLASTX
NCBI GI      g3345477
BLAST score   544
E value      9.0e-56
Match length  142
% identity    75
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
```

Seq. No.	399145
Seq. ID	LIB3431-022-P1-K1-A9
Method	BLASTX
NCBI GI	g2245086
BLAST score	373
E value	1.0e-35
Match length	104
% identity	68
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

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00684016-101000

Match length	84
% identity	67
NCBI Description	(AC004557) F17L21.18 [Arabidopsis thaliana]
Seq. No.	399163
Seq. ID	LIB3431-022-P1-K1-D12
Method	BLASTX
NCBI GI	g3789954
BLAST score	661
E value	2.0e-69
Match length	125
% identity	98
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]
Seq. No.	399164
Seq. ID	LIB3431-022-P1-K1-D4
Method	BLASTX
NCBI GI	g320618
BLAST score	593
E value	2.0e-61
Match length	130
% identity	87
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf_1707316A chlorophyll a/b binding protein 1 [Oryza sativa]
Seq. No.	399165
Seq. ID	LIB3431-022-P1-K1-D5
Method	BLASTX
NCBI GI	g4099148
BLAST score	582
E value	3.0e-60
Match length	147
% identity	82
NCBI Description	(U84268) YLP [Hordeum vulgare]
Seq. No.	399166
Seq. ID	LIB3431-022-P1-K1-D6
Method	BLASTX
NCBI GI	g2293288
BLAST score	175
E value	2.0e-12
Match length	152
% identity	33
NCBI Description	(AF008220) YtcB [Bacillus subtilis] >gi_2635571_emb_CAB15065_ (Z99119) similar to NDP-sugar epimerase [Bacillus subtilis]
Seq. No.	399167
Seq. ID	LIB3431-022-P1-K1-D7
Method	BLASTX
NCBI GI	g5106775
BLAST score	488
E value	3.0e-49

Seq. No.	399178
Seq. ID	LIB3431-022-P1-K1-E9
Method	BLASTN
NCBI GI	g3075487
BLAST score	322
E value	0.0e+00
Match length	322
% identity	100
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

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Seq. No.      399179
Seq. ID      LIB3431-022-P1-K1-F10
Method       BLASTX
NCBI GI      g2493494
BLAST score   547
E value      4.0e-56
Match length  112
% identity    89
NCBI Description SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2)
                >gi_619351_bbs_153537 CP-MII.2=serine carboxypeptidase
                [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436
                aa] >gi_6102957_emb_CAB59202.1_ (X78878) serine carboxylase
                II-2 [Hordeum vulgare]
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Seq. No.      399180
Seq. ID      LIB3431-022-P1-K1-F11
Method       BLASTX
NCBI GI      g115787
BLAST score   584
E value      2.0e-60
Match length  133
% identity    88
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
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```
Seq. No.      399181
Seq. ID      LIB3431-022-P1-K1-F12
Method       BLASTX
NCBI GI      g3618310
BLAST score   473
E value      2.0e-47
Match length  123
% identity    74
NCBI Description (AB001883) zinc finger protein [Oryza sativa]
```

Seq. No.	399182
Seq. ID	LIB3431-022-P1-K1-F2
Method	BLASTX
NCBI GI	g710626
BLAST score	188
E value	5.0e-14
Match length	45
% identity	69

chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 399188
 Seq. ID LIB3431-022-P1-K1-F9
 Method BLASTX
 NCBI GI g5295954
 BLAST score 363
 E value 2.0e-34
 Match length 72
 % identity 97
 NCBI Description (AB026295) hypothetical protein [Oryza sativa]

Seq. No. 399189
 Seq. ID LIB3431-022-P1-K1-G10
 Method BLASTX
 NCBI GI g320618
 BLAST score 622
 E value 7.0e-65
 Match length 135
 % identity 87
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 399190
 Seq. ID LIB3431-022-P1-K1-G12
 Method BLASTN
 NCBI GI g2062705
 BLAST score 35
 E value 5.0e-10
 Match length 35
 % identity 100
 NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 399191
 Seq. ID LIB3431-022-P1-K1-G4
 Method BLASTX
 NCBI GI g120657
 BLAST score 528
 E value 6.0e-54
 Match length 132
 % identity 81
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
 CHLOROPLAST >gi_66024_pir_DEZMG3
 glyceraldehyde-3-phosphate dehydrogenase (NADP+)
 (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
 maize >gi_168479 (M18976) glyceraldehyde-3-phosphate
 dehydrogenase [Zea mays] >gi_763035_emb_CAA33455_ (X15408)
 glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

Seq. No. 399192
 Seq. ID LIB3431-022-P1-K1-G5
 Method BLASTX


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Method          BLASTX
NCBI GI         g1171978
BLAST score     418
E value         4.0e-45
Match length    128
% identity      63
NCBI Description POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)
                  (PABP 2) >gi_304109 (L19418) poly(A)-binding protein
                  [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961)
                  poly(A)-binding protein [Arabidopsis thaliana]

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Seq. No.      399198
Seq. ID       LIB3431-022-P1-K1-H12
Method        BLASTX
NCBI GI       g3345477
BLAST score   317
E value       3.0e-29
Match length  115
% identity    57
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
```

[illegible]

```
Seq. No.      399200
Seq. ID      LIB3431-022-P1-K1-H4
Method       BLASTX
NCBI GI      g3184559
BLAST score   289
E value      7.0e-26
Match length  128
% identity    50
NCBI Description (AF052290) putative c-type cytochrome biogenesis protein
               [Synechococcus PCC7002]
```

```
Seq. No.      399201
Seq. ID      LIB3431-022-P1-K1-H6
Method       BLASTX
NCBI GI      g3510256
BLAST score   180
E value      3.0e-13
Match length  41
% identity    78
NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]
```

Seq. No. 399202
 Seq. ID LIB3431-022-P1-K1-H7
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 8.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 399203
 Seq. ID LIB3431-022-P1-K1-H8
 Method BLASTX
 NCBI GI g3126854
 BLAST score 730
 E value 1.0e-77
 Match length 139
 % identity 99
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 399204
 Seq. ID LIB3431-022-P1-N1-A1
 Method BLASTX
 NCBI GI g671740
 BLAST score 202
 E value 1.0e-15
 Match length 51
 % identity 80
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
 construct]

Seq. No. 399205
 Seq. ID LIB3431-022-P1-N1-A4
 Method BLASTX
 NCBI GI g3885892
 BLAST score 235
 E value 1.0e-19
 Match length 47
 % identity 98
 NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 399206
 Seq. ID LIB3431-022-P1-N1-A5
 Method BLASTX
 NCBI GI g671740
 BLAST score 197
 E value 3.0e-15
 Match length 37
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
 construct]

Seq. No. 399207
 Seq. ID LIB3431-022-P1-N1-A6
 Method BLASTN

Method	BLASTN
NCBI GI	g3075487
BLAST score	42
E value	3.0e-14
Match length	82
% identity	88
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds
Seq. No.	399213
Seq. ID	LIB3431-022-P1-N1-B2
Method	BLASTN
NCBI GI	g218209
BLAST score	159
E value	5.0e-84
Match length	304
% identity	97
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106
Seq. No.	399214
Seq. ID	LIB3431-022-P1-N1-B3
Method	BLASTX
NCBI GI	g4982498
BLAST score	187
E value	5.0e-14
Match length	59
% identity	59
NCBI Description	(AC000107) F17F8.4 [Arabidopsis thaliana]
Seq. No.	399215
Seq. ID	LIB3431-022-P1-N1-B5
Method	BLASTN
NCBI GI	g3789951
BLAST score	168
E value	2.0e-89
Match length	374
% identity	93
NCBI Description	Oryza sativa chlorophyll a/b-binding protein precursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds
Seq. No.	399216
Seq. ID	LIB3431-022-P1-N1-B7
Method	BLASTX
NCBI GI	g132105
BLAST score	402
E value	4.0e-39
Match length	73
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538 (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)

E value 2.0e-24
 Match length 54
 % identity 98
 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein
 [Nicotiana sylvestris]

Seq. No. 399243
 Seq. ID LIB3431-022-P1-N1-F9
 Method BLASTN
 NCBI GI g5295936
 BLAST score 310
 E value 1.0e-174
 Match length 411
 % identity 94
 NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0681F10,
 complete sequence

Seq. No. 399244
 Seq. ID LIB3431-022-P1-N1-G10
 Method BLASTX
 NCBI GI g3928150
 BLAST score 412
 E value 3.0e-40
 Match length 110
 % identity 72
 NCBI Description (AJ131049) hypothetical protein [Cicer arietinum]

Seq. No. 399245
 Seq. ID LIB3431-022-P1-N1-G4
 Method BLASTX
 NCBI GI g120661
 BLAST score 178
 E value 6.0e-13
 Match length 32
 % identity 100
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST
 PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate
 dehydrogenase A-subunit precursor [Nicotiana tabacum]

Seq. No. 399246
 Seq. ID LIB3431-022-P1-N1-G6
 Method BLASTX
 NCBI GI g347451
 BLAST score 263
 E value 7.0e-23
 Match length 51
 % identity 100
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
 sativa]

Seq. No. 399247
 Seq. ID LIB3431-022-P1-N1-H11
 Method BLASTX
 NCBI GI g2213871
 BLAST score 195
 E value 7.0e-15
 Match length 53

% identity 83
NCBI Description (AF003126) poly(A)-binding protein [Mesembryanthemum crystallinum]

Seq. No. 399248
Seq. ID LIB3431-022-P1-N1-H12
Method BLASTX
NCBI GI g3345477
BLAST score 156
E value 2.0e-10
Match length 30
% identity 97
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 399249
Seq. ID LIB3431-022-P1-N1-H2
Method BLASTX
NCBI GI g1707998
BLAST score 153
E value 5.0e-10
Match length 29
% identity 100
NCBI Description SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_481944_pir_S40218 glycine hydroxymethyltransferase (EC 2.1.2.1) - potato >gi_438247_emb_CAA81082_ (Z25863) glycine hydroxymethyltransferase [Solanum tuberosum]

Seq. No. 399250
Seq. ID LIB3431-022-P1-N1-H6
Method BLASTX
NCBI GI g3510256
BLAST score 167
E value 1.0e-11
Match length 41
% identity 73
NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]

Seq. No. 399251
Seq. ID LIB3431-022-P1-N1-H7
Method BLASTN
NCBI GI g2072554
BLAST score 310
E value 1.0e-174
Match length 322
% identity 99
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 399252
Seq. ID LIB3431-022-P1-N1-H8
Method BLASTX
NCBI GI g115802
BLAST score 190
E value 2.0e-14
Match length 35

Method BLASTX
 NCBI GI g2147484
 BLAST score 592
 E value 2.0e-61
 Match length 137
 % identity 81
 NCBI Description homeotic protein - Phalaenopsis sp >gi_1173622 (U34743)
 homeobox protein [Phalaenopsis sp. 'hybrid SM9108']

Seq. No. 399268
 Seq. ID LIB3431-023-P1-K1-B9
 Method BLASTX
 NCBI GI g2660676
 BLAST score 614
 E value 5.0e-64
 Match length 134
 % identity 81
 NCBI Description (AC002342) Dreg-2 like protein [Arabidopsis thaliana]

Seq. No. 399269
 Seq. ID LIB3431-023-P1-K1-C1
 Method BLASTX
 NCBI GI g6006848
 BLAST score 405
 E value 2.0e-45
 Match length 141
 % identity 67
 NCBI Description (AC009540) unknown protein, 5' partial [Arabidopsis thaliana]

Seq. No. 399270
 Seq. ID LIB3431-023-P1-K1-C11
 Method BLASTN
 NCBI GI g2306980
 BLAST score 53
 E value 7.0e-21
 Match length 85
 % identity 91
 NCBI Description Oryza sativa photosystem I antenna protein (Lhca) mRNA, complete cds

Seq. No. 399271
 Seq. ID LIB3431-023-P1-K1-C12
 Method BLASTX
 NCBI GI g132105
 BLAST score 607
 E value 4.0e-63
 Match length 132
 % identity 87
 NCBI Description RIBULOSE BISPHTOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate

E value 5.0e-36
 Match length 95
 % identity 75
 NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]
 >gi_4874312_gb_AAD31374.1_AC006053_16 (AC006053)
 hypothetical protein [Arabidopsis thaliana]

Seq. No. 399277
 Seq. ID LIB3431-023-P1-K1-C8
 Method BLASTX
 NCBI GI g4803952
 BLAST score 284
 E value 3.0e-25
 Match length 69
 % identity 77
 NCBI Description (AC006202) hypothetical protein [Arabidopsis thaliana]

Seq. No. 399278
 Seq. ID LIB3431-023-P1-K1-C9
 Method BLASTX
 NCBI GI g4455350
 BLAST score 322
 E value 1.0e-29
 Match length 79
 % identity 81
 NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 399279
 Seq. ID LIB3431-023-P1-K1-D1
 Method BLASTX
 NCBI GI g2052383
 BLAST score 403
 E value 3.0e-39
 Match length 86
 % identity 80
 NCBI Description (U66345) calreticulin [Arabidopsis thaliana]

Seq. No. 399280
 Seq. ID LIB3431-023-P1-K1-D10
 Method BLASTX
 NCBI GI g3885892
 BLAST score 440
 E value 1.0e-43
 Match length 83
 % identity 100
 NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 399281
 Seq. ID LIB3431-023-P1-K1-D11
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 399282
 Seq. ID LIB3431-023-P1-K1-D2
 Method BLASTX
 NCBI GI g5816996
 BLAST score 406
 E value 1.0e-39
 Match length 85
 % identity 91
 NCBI Description (AL110123) ribosomal protein L32-like protein [Arabidopsis thaliana]

Seq. No. 399283
 Seq. ID LIB3431-023-P1-K1-D3
 Method BLASTX
 NCBI GI g132105
 BLAST score 560
 E value 1.0e-57
 Match length 122
 % identity 86
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 399284
 Seq. ID LIB3431-023-P1-K1-D5
 Method BLASTX
 NCBI GI g5816996
 BLAST score 282
 E value 5.0e-25
 Match length 61
 % identity 90
 NCBI Description (AL110123) ribosomal protein L32-like protein [Arabidopsis thaliana]

Seq. No. 399285
 Seq. ID LIB3431-023-P1-K1-D8
 Method BLASTX
 NCBI GI g4914457
 BLAST score 392
 E value 6.0e-38
 Match length 122
 % identity 55
 NCBI Description (AL050400) putative protein [Arabidopsis thaliana]

Seq. No. 399286
 Seq. ID LIB3431-023-P1-K1-E1
 Method BLASTX
 NCBI GI g3929924
 BLAST score 620

Seq. No. 399301
 Seq. ID LIB3431-023-P1-K1-G12
 Method BLASTX
 NCBI GI g2501190
 BLAST score 591
 E value 3.0e-61
 Match length 140
 % identity 84
 NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
 >gi_2130147_pir_S61420 thiamine biosynthetic enzyme thil-2
 - maize >gi_596080 (U17351) thiamine biosynthetic enzyme
 [Zea mays]

Seq. No. 399302
 Seq. ID LIB3431-023-P1-K1-G2
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 399303
 Seq. ID LIB3431-023-P1-K1-G3
 Method BLASTX
 NCBI GI g4079798
 BLAST score 558
 E value 2.0e-57
 Match length 143
 % identity 78
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza
 sativa]

Seq. No. 399304
 Seq. ID LIB3431-023-P1-K1-G5
 Method BLASTX
 NCBI GI g66298
 BLAST score 347
 E value 9.0e-36
 Match length 87
 % identity 84
 NCBI Description catalase (EC 1.11.1.6) - rice >gi_20192_emb_CAA43814_
 (X61626) catalase [Oryza sativa]

Seq. No. 399305
 Seq. ID LIB3431-023-P1-K1-G7
 Method BLASTX
 NCBI GI g4972093
 BLAST score 263
 E value 9.0e-23
 Match length 116
 % identity 47
 NCBI Description (AL078468) putative protein [Arabidopsis thaliana]

00664015-101000

Seq. No. 399320
Seq. ID LIB3431-023-P1-N1-A6
Method BLASTN
NCBI GI g304219
BLAST score 36
E value 5.0e-11
Match length 68
% identity 88
NCBI Description Hordeum vulgare chloroplast photosystem I PSK-I subunit mRNA, complete cds

Seq. No. 399321
Seq. ID LIB3431-023-P1-N1-B2
Method BLASTX
NCBI GI g347451
BLAST score 207
E value 3.0e-16
Match length 39
% identity 100
NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 399322
Seq. ID LIB3431-023-P1-N1-B5
Method BLASTN
NCBI GI g3885887
BLAST score 164
E value 4.0e-87
Match length 272
% identity 90
NCBI Description Oryza sativa high mobility group protein (HMG) mRNA, complete cds

Seq. No. 399323
Seq. ID LIB3431-023-P1-N1-C11
Method BLASTX
NCBI GI g1076724
BLAST score 263
E value 7.0e-23
Match length 56
% identity 88
NCBI Description LHCI-680, photosystem I antenna protein - barley
>gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I antenna protein [Hordeum vulgare]

Seq. No. 399324
Seq. ID LIB3431-023-P1-N1-C12
Method BLASTX
NCBI GI g671740
BLAST score 546
E value 7.0e-56
Match length 99
% identity 100
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No.	399325
Seq. ID	LIB3431-023-P1-N1-C2
Method	BLASTX
NCBI GI	g231610
BLAST score	215
E value	3.0e-17
Match length	65
% identity	74
NCBI Description	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi_67880_pir_PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase (gamma subunit) [Nicotiana tabacum]
Seq. No.	399326
Seq. ID	LIB3431-023-P1-N1-C3
Method	BLASTN
NCBI GI	g606816
BLAST score	301
E value	1.0e-169
Match length	321
% identity	98
NCBI Description	Oryza sativa chloroplast carbonic anhydrase mRNA, complete cds
Seq. No.	399327
Seq. ID	LIB3431-023-P1-N1-C4
Method	BLASTN
NCBI GI	g2072554
BLAST score	403
E value	0.0e+00
Match length	403
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds
Seq. No.	399328
Seq. ID	LIB3431-023-P1-N1-C5
Method	BLASTX
NCBI GI	g3183079
BLAST score	629
E value	1.0e-65
Match length	147
% identity	82
NCBI Description	MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR >gi_1375075_dbj_BAA12870.1_ (D85763) glyoxysomal malate dehydrogenase [Oryza sativa]
Seq. No.	399329
Seq. ID	LIB3431-023-P1-N1-C9
Method	BLASTX
NCBI GI	g731707
BLAST score	204
E value	2.0e-22
Match length	116
% identity	47
NCBI Description	SET1 PROTEIN >gi_626647_pir_S48961 hypothetical protein

Seq. No. 399344
 Seq. ID LIB3431-023-P1-N1-F5
 Method BLASTX
 NCBI GI g115794
 BLAST score 467
 E value 9.0e-47
 Match length 94
 % identity 91
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE III CAB-13) >gi_72748_pir_CDT033 chlorophyll a/b-binding protein type III precursor (cab-13) - tomato
 >gi_19277_emb_CAA42818_ (X60275) LHCII type III [Lycopersicon esculentum]

Seq. No. 399345
 Seq. ID LIB3431-023-P1-N1-F6
 Method BLASTX
 NCBI GI g547712
 BLAST score 219
 E value 1.0e-17
 Match length 43
 % identity 100
 NCBI Description EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)
 >gi_542153_pir_S38358 translation initiation factor eIF-4A - rice >gi_303844_dbj_BAA02152_ (D12627) eukaryotic initiation factor 4A [Oryza sativa]

Seq. No. 399346
 Seq. ID LIB3431-023-P1-N1-F7
 Method BLASTX
 NCBI GI g347451
 BLAST score 169
 E value 8.0e-12
 Match length 32
 % identity 100
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 399347
 Seq. ID LIB3431-023-P1-N1-F9
 Method BLASTX
 NCBI GI g134034
 BLAST score 238
 E value 6.0e-20
 Match length 66
 % identity 68
 NCBI Description 30S RIBOSOMAL PROTEIN S30, CHLOROPLAST PRECURSOR (CS-S5) (CS5) (S22) (RIBOSOMAL PROTEIN 1) (PSRP-1)
 >gi_279640_pir_R3SPS5 ribosomal protein CS-S22 precursor, chloroplast - spinach >gi_12316_emb_CAA41960_ (X59270) chloroplast ribosomal protein S22 [Spinacia oleracea]
 >gi_18031_emb_CAA33403_ (X15344) spinach S22 r-protein [Spinacia oleracea]

Seq. No. 399348
 Seq. ID LIB3431-023-P1-N1-G10
 Method BLASTX

NCBI GI g421916
 BLAST score 199
 E value 2.0e-15
 Match length 37
 % identity 100
 NCBI Description chlorophyll a/b-binding protein - English ivy (fragment)
 >gi_12582_emb_CAA48410_ (X68333) light harvesting
 chlorophyll a /b binding protein [Hedera helix]

Seq. No. 399349
 Seq. ID LIB3431-023-P1-N1-G2
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 399350
 Seq. ID LIB3431-023-P1-N1-G5
 Method BLASTX
 NCBI GI g2130069
 BLAST score 192
 E value 2.0e-14
 Match length 39
 % identity 95
 NCBI Description catalase (EC 1.11.1.6) catA - rice
 >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]

Seq. No. 399351
 Seq. ID LIB3431-023-P1-N1-G7
 Method BLASTX
 NCBI GI g4972093
 BLAST score 236
 E value 1.0e-19
 Match length 59
 % identity 76
 NCBI Description (AL078468) putative protein [Arabidopsis thaliana]

Seq. No. 399352
 Seq. ID LIB3431-023-P1-N1-G8
 Method BLASTX
 NCBI GI g3789954
 BLAST score 329
 E value 1.0e-30
 Match length 62
 % identity 98
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 399353
 Seq. ID LIB3431-023-P1-N1-G9
 Method BLASTX
 NCBI GI g132105

Seq. No. 399363
 Seq. ID LIB3431-024-P1-K1-A4
 Method BLASTN
 NCBI GI g487319
 BLAST score 47
 E value 3.0e-17
 Match length 47
 % identity 100
 NCBI Description Rice mRNA EN66, partial sequence

Seq. No. 399364
 Seq. ID LIB3431-024-P1-K1-A7
 Method BLASTX
 NCBI GI g5902390
 BLAST score 174
 E value 2.0e-12
 Match length 119
 % identity 40
 NCBI Description (AC008148) Unknown protein [Arabidopsis thaliana]

Seq. No. 399365
 Seq. ID LIB3431-024-P1-K1-A9
 Method BLASTX
 NCBI GI g2407281
 BLAST score 673
 E value 6.0e-71
 Match length 125
 % identity 99
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 399366
 Seq. ID LIB3431-024-P1-K1-B1
 Method BLASTX
 NCBI GI g132105
 BLAST score 530
 E value 4.0e-54
 Match length 96
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 399367
 Seq. ID LIB3431-024-P1-K1-B10
 Method BLASTX
 NCBI GI g729478
 BLAST score 343
 E value 3.0e-32
 Match length 119

Method	BLASTX
NCBI GI	g4689380
BLAST score	620
E value	9.0e-65
Match length	125
% identity	88
NCBI Description	(AF139465) LHCII type III chlorophyll a/b binding protein [Vigna radiata]
Seq. No.	399388
Seq. ID	LIB3431-024-P1-K1-D12
Method	BLASTX
NCBI GI	g320618
BLAST score	463
E value	2.0e-46
Match length	106
% identity	83
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_(D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf_1707316A chlorophyll a/b binding protein 1 [Oryza sativa]
Seq. No.	399389
Seq. ID	LIB3431-024-P1-K1-D2
Method	BLASTN
NCBI GI	g2306980
BLAST score	150
E value	7.0e-79
Match length	174
% identity	97
NCBI Description	Oryza sativa photosystem I antenna protein (Lhca) mRNA, complete cds
Seq. No.	399390
Seq. ID	LIB3431-024-P1-K1-D3
Method	BLASTX
NCBI GI	g871931
BLAST score	361
E value	1.0e-36
Match length	85
% identity	100
NCBI Description	(D30763) ferredoxin [Oryza sativa]
Seq. No.	399391
Seq. ID	LIB3431-024-P1-K1-D4
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	4.0e-10
Match length	35
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds
Seq. No.	399392
Seq. ID	LIB3431-024-P1-K1-D6
Method	BLASTX

NCBI GI	g2342719
BLAST score	324
E value	6.0e-30
Match length	139
% identity	50
NCBI Description	(AC002341) SF16 protein isolog [Arabidopsis thaliana]
Seq. No.	399393
Seq. ID	LIB3431-024-P1-K1-D9
Method	BLASTX
NCBI GI	g4585882
BLAST score	399
E value	7.0e-39
Match length	127
% identity	62
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]
Seq. No.	399394
Seq. ID	LIB3431-024-P1-K1-E1
Method	BLASTX
NCBI GI	g2407281
BLAST score	547
E value	3.0e-56
Match length	108
% identity	96
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]
Seq. No.	399395
Seq. ID	LIB3431-024-P1-K1-E10
Method	BLASTX
NCBI GI	g133936
BLAST score	685
E value	3.0e-72
Match length	132
% identity	100
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi_70867_pir__R3RZ3 ribosomal protein S3 - rice chloroplast >gi_12025_emb_CAA33934_(X15901) ribosomal protein S3 [Oryza sativa] >gi_226646_prf__1603356BW ribosomal protein S3 [Oryza sativa]
Seq. No.	399396
Seq. ID	LIB3431-024-P1-K1-E12
Method	BLASTX
NCBI GI	g2130069
BLAST score	749
E value	8.0e-80
Match length	135
% identity	99
NCBI Description	catalase (EC 1.11.1.6) cataA - rice >gi_1261858_dbj_BAA06232_(D29966) catalase [Oryza sativa]
Seq. No.	399397
Seq. ID	LIB3431-024-P1-K1-E2
Method	BLASTX


```
Method          BLASTX
NCBI GI         g5902158
BLAST score     246
E value        6.0e-21
Match length    75
% identity      56
NCBI Description zinc finger protein 183 (RING finger, C3HC4 type)
                >gi_3123165_sp_015541_z183_HUMAN_ZINC_FINGER_PROTEIN_183
                >gi_2274982_emb_CAA66907_(X98253) ZNF183 [Homo sapiens]
                >gi_2341022_(AC002477) zinc-finger protein [Homo sapiens]
```

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Seq. No.      399414
Seq. ID      LIB3431-024-P1-K1-G2
Method       BLASTX
NCBI GI      g2072555
BLAST score   237
E value      6.0e-20
Match length  44
% identity    100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
                >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                protein [Oryza sativa]
```

```
Seq. No.      399415
Seq. ID      LIB3431-024-P1-K1-G4
Method       BLASTX
NCBI GI      g115787
BLAST score   380
E value      1.0e-36
Match length  92
% identity    85
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
```

Seq. No.	399416
Seq. ID	LIB3431-024-P1-K1-G6
Method	BLASTX
NCBI GI	g1657859
BLAST score	155
E value	2.0e-10
Match length	60
% identity	55
NCBI Description	(U73218) chlorophyll a/b-binding protein WCAB precursor [Triticum aestivum]

Seq. No.	399417
Seq. ID	LIB3431-024-P1-K1-G7
Method	BLASTX
NCBI GI	g3386621
BLAST score	554
E value	6.0e-57
Match length	147
% identity	71
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 399418
 Seq. ID LIB3431-024-P1-K1-G8
 Method BLASTX
 NCBI GI g4538947
 BLAST score 166
 E value 1.0e-11
 Match length 61
 % identity 54
 NCBI Description (AL049483) putative mitochondrial carrier protein
 [Arabidopsis thaliana]

Seq. No. 399419
 Seq. ID LIB3431-024-P1-K1-G9
 Method BLASTX
 NCBI GI g132105
 BLAST score 289
 E value 4.0e-26
 Match length 76
 % identity 78
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 399420
 Seq. ID LIB3431-024-P1-K1-H1
 Method BLASTX
 NCBI GI g3885886
 BLAST score 327
 E value 8.0e-31
 Match length 65
 % identity 100
 NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]

Seq. No. 399421
 Seq. ID LIB3431-024-P1-K1-H11
 Method BLASTX
 NCBI GI g1931644
 BLAST score 250
 E value 3.0e-21
 Match length 105
 % identity 44
 NCBI Description (U95973) membrane protein PTM1 precursor isolog
 [Arabidopsis thaliana]

Seq. No. 399422
 Seq. ID LIB3431-024-P1-K1-H12
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 8.0e-20

Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 399423
 Seq. ID LIB3431-024-P1-K1-H2
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 6.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 399424
 Seq. ID LIB3431-024-P1-K1-H3
 Method BLASTX
 NCBI GI g1835731
 BLAST score 189
 E value 3.0e-14
 Match length 49
 % identity 76
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 399425
 Seq. ID LIB3431-024-P1-K1-H4
 Method BLASTX
 NCBI GI g1498315
 BLAST score 250
 E value 7.0e-25
 Match length 121
 % identity 50
 NCBI Description (U56419) IAP100 [Pisum sativum]

Seq. No. 399426
 Seq. ID LIB3431-024-P1-K1-H5
 Method BLASTX
 NCBI GI g1617197
 BLAST score 290
 E value 6.0e-26
 Match length 76
 % identity 74
 NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 399427
 Seq. ID LIB3431-024-P1-K1-H6
 Method BLASTN
 NCBI GI g3821780
 BLAST score 34
 E value 9.0e-10
 Match length 34
 % identity 100
 NCBI Description Xenopus laevis cDNA clone 27A6-1

BLAST score 370
 E value 2.0e-35
 Match length 73
 % identity 92
 NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
 >gi_442481_dbj_BAA04616 (D17790) ferredoxin-NADP+
 reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1
 (AP000616) ESTs AU078647(E1557), C72400(E1557) correspond to
 a region of the predicted gene.; similar to
 ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

Seq. No. 399433
 Seq. ID LIB3431-024-P1-N1-B12
 Method BLASTX
 NCBI GI g132166
 BLAST score 156
 E value 2.0e-10
 Match length 31
 % identity 84
 NCBI Description RIBULOSE BISPHTHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
 CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
 >gi_81660_pir_S04048 ribulose-bisphosphate carboxylase
 activase precursor - Arabidopsis thaliana
 >gi_16471_emb_CAA32429 (X14212) rubisco activase (AA 1 -
 473) [Arabidopsis thaliana]

Seq. No. 399434
 Seq. ID LIB3431-024-P1-N1-B2
 Method BLASTX
 NCBI GI g417260
 BLAST score 268
 E value 2.0e-23
 Match length 69
 % identity 72
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

Seq. No. 399435
 Seq. ID LIB3431-024-P1-N1-B4
 Method BLASTX
 NCBI GI g3789954
 BLAST score 335
 E value 3.0e-31
 Match length 62
 % identity 100
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza
 sativa]

Seq. No. 399436
 Seq. ID LIB3431-024-P1-N1-B5
 Method BLASTX
 NCBI GI g131225
 BLAST score 196
 E value 5.0e-15
 Match length 51
 % identity 73

0001016-101000

BLAST score 216
E value 2.0e-17
Match length 44
% identity 100
NCBI Description (AF017362) aldolase [Oryza sativa]

Seq. No. 399442
Seq. ID LIB3431-024-P1-N1-C11
Method BLASTX
NCBI GI g3036946
BLAST score 319
E value 2.0e-29
Match length 61
% identity 100
NCBI Description (AB012637) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 399443
Seq. ID LIB3431-024-P1-N1-C12
Method BLASTX
NCBI GI g1835731
BLAST score 188
E value 3.0e-14
Match length 48
% identity 77
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 399444
Seq. ID LIB3431-024-P1-N1-C3
Method BLASTX
NCBI GI g3036942
BLAST score 243
E value 1.0e-20
Match length 45
% identity 100
NCBI Description (AB012636) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 399445
Seq. ID LIB3431-024-P1-N1-C8
Method BLASTN
NCBI GI g2072554
BLAST score 246
E value 1.0e-136
Match length 282
% identity 97
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 399446
Seq. ID LIB3431-024-P1-N1-D1
Method BLASTX
NCBI GI g3913641
BLAST score 211
E value 4.0e-17
Match length 41
% identity 100

0968-0167

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Seq. No.      399458
Seq. ID      LIB3431-024-P1-N1-E8
Method       BLASTX
NCBI GI      g3126854
BLAST score   240
E value      3.0e-20
Match length  65
% identity   74
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```

```
Seq. No.      399460
Seq. ID      LIB3431-024-P1-N1-F10
Method       BLASTX
NCBI GI      g3126854
BLAST score   261
E value      1.0e-22
Match length  52
% identity    94
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```

```
Seq. No.      399462
Seq. ID       LIB3431-024-P1-N1-F2
Method        BLASTN
NCBI GI       q5360229
```

BLAST score 394
 E value 0.0e+00
 Match length 419
 % identity 98
 NCBI Description Oryza sativa mRNA for Ran, complete cds

Seq. No. 399463
 Seq. ID LIB3431-024-P1-N1-F3
 Method BLASTN
 NCBI GI g3789949
 BLAST score 83
 E value 1.0e-38
 Match length 95
 % identity 97
 NCBI Description Oryza sativa translation initiation factor (GOS2) mRNA, complete cds

Seq. No. 399464
 Seq. ID LIB3431-024-P1-N1-F4
 Method BLASTX
 NCBI GI g4582436
 BLAST score 162
 E value 7.0e-11
 Match length 77
 % identity 47
 NCBI Description (AC007196) unknown protein [Arabidopsis thaliana]

Seq. No. 399465
 Seq. ID LIB3431-024-P1-N1-F7
 Method BLASTX
 NCBI GI g4929312
 BLAST score 203
 E value 7.0e-16
 Match length 70
 % identity 63
 NCBI Description (AF145045) TATC [Arabidopsis thaliana]

Seq. No. 399466
 Seq. ID LIB3431-024-P1-N1-G10
 Method BLASTX
 NCBI GI g4731573
 BLAST score 201
 E value 1.0e-15
 Match length 48
 % identity 77
 NCBI Description (AF123265) remorin 1 [Lycopersicon esculentum]

Seq. No. 399467
 Seq. ID LIB3431-024-P1-N1-G12
 Method BLASTX
 NCBI GI g5262156
 BLAST score 226
 E value 2.0e-18
 Match length 65
 % identity 52
 NCBI Description (AL080237) putative protein [Arabidopsis thaliana]

09654010 101000

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Seq. No.      399474
Seq. ID      LIB3431-024-P1-N1-H12
Method       BLASTX
NCBI GI      g2072555
BLAST score   237
E value      9.0e-20
Match length  44
% identity    100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
protein [Oryza sativa]
```

Seq. No.	399476
Seq. ID	LIB3431-024-P1-N1-H3
Method	BLASTX
NCBI GI	g1835731
BLAST score	189
E value	3.0e-14
Match length	49
% identity	78
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 399483
 Seq. ID LIB3431-025-P1-K1-A8
 Method BLASTX
 NCBI GI g2501491
 BLAST score 182
 E value 1.0e-13
 Match length 90
 % identity 42
 NCBI Description FLAVONOL 3-O-GLUCOSYLTRANSFERASE 1 (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE 1) >gi_542014_pir__S41950
 UTP-glucose glucosyltransferase - cassava
 >gi_453246_emb_CAA54609_(X77459) UTP-glucose
 glucosyltransferase [Manihot esculenta]

Seq. No. 399484
 Seq. ID LIB3431-025-P1-K1-B11
 Method BLASTX
 NCBI GI g671740
 BLAST score 433
 E value 1.0e-42
 Match length 79
 % identity 99
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
 construct]

Seq. No. 399485
 Seq. ID LIB3431-025-P1-K1-B2
 Method BLASTX
 NCBI GI g1362184
 BLAST score 447
 E value 4.0e-44
 Match length 91
 % identity 100
 NCBI Description histone H2B-8 - wheat >gi_531058_dbj_BAA07157_(D37943)
 protein H2B-8 [Triticum aestivum]

Seq. No. 399486
 Seq. ID LIB3431-025-P1-K1-B3
 Method BLASTX
 NCBI GI g1076800
 BLAST score 681
 E value 1.0e-71
 Match length 148
 % identity 86
 NCBI Description L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -
 maize >gi_600116_emb_CAA84406_(Z34934) cytosolic ascorbate
 peroxidase [Zea mays] >gi_1096503_prf__2111423A ascorbate
 peroxidase [Zea mays]

Seq. No. 399487
 Seq. ID LIB3431-025-P1-K1-B5
 Method BLASTX
 NCBI GI g3868756
 BLAST score 842
 E value 2.0e-90
 Match length 154
 % identity 100

Seq. No. 399498
 Seq. ID LIB3431-025-P1-K1-D8
 Method BLASTX
 NCBI GI g2055273
 BLAST score 1024
 E value 1.0e-112
 Match length 236
 % identity 83
 NCBI Description (D85339) hydroxypyruvate reductase [Arabidopsis thaliana]

Seq. No. 399499
 Seq. ID LIB3431-025-P1-K1-D9
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 1.0e-19
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 399500
 Seq. ID LIB3431-025-P1-K1-E11
 Method BLASTX
 NCBI GI g347451
 BLAST score 459
 E value 1.0e-57
 Match length 165
 % identity 74
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 399501
 Seq. ID LIB3431-025-P1-K1-E12
 Method BLASTX
 NCBI GI g2582822
 BLAST score 606
 E value 7.0e-63
 Match length 168
 % identity 71
 NCBI Description (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]

Seq. No. 399502
 Seq. ID LIB3431-025-P1-K1-E5
 Method BLASTX
 NCBI GI g462195
 BLAST score 524
 E value 4.0e-53
 Match length 115
 % identity 89
 NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
 >gi_100682_pir_S21636 GOS2 protein - rice
 >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
 >gi_3789950 (AF094774) translation initiation factor [Oryza

sativa]

Seq. No. 399503
 Seq. ID LIB3431-025-P1-K1-E6
 Method BLASTX
 NCBI GI g2425101
 BLAST score 798
 E value 3.0e-85
 Match length 215
 % identity 64
 NCBI Description (AF019743) cationic peroxidase [Oryza sativa]

Seq. No. 399504
 Seq. ID LIB3431-025-P1-K1-E7
 Method BLASTN
 NCBI GI g1841354
 BLAST score 66
 E value 2.0e-29
 Match length 66
 % identity 100
 NCBI Description Oryza sativa mitochondrial DNA for cytochrome c oxidase subunit Vb precursor, complete cds

Seq. No. 399505
 Seq. ID LIB3431-025-P1-K1-E9
 Method BLASTX
 NCBI GI g3913239
 BLAST score 406
 E value 2.0e-39
 Match length 146
 % identity 58
 NCBI Description PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE (DXP SYNTHASE) >gi_2612941 (AF024512) CLA1 transketolase-like protein [Oryza sativa]

Seq. No. 399506
 Seq. ID LIB3431-025-P1-K1-F10
 Method BLASTX
 NCBI GI g1084455
 BLAST score 503
 E value 8.0e-51
 Match length 118
 % identity 81
 NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]

Seq. No. 399507
 Seq. ID LIB3431-025-P1-K1-F11
 Method BLASTX
 NCBI GI g1777961
 BLAST score 958
 E value 1.0e-104
 Match length 233
 % identity 76
 NCBI Description (U56406) methyljasmonate-inducible lipoxygenase 2 [Hordeum vulgare]

Seq. No. 399508
 Seq. ID LIB3431-025-P1-K1-F12
 Method BLASTX
 NCBI GI g400803
 BLAST score 509
 E value 3.0e-64
 Match length 154
 % identity 82
 NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi_283033_pir_A42807 phosphoglycerate mutase (EC 5.4.2.1), 2, 3-bisphosphoglycerate-independent - maize >gi_168588 (M80912) 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Zea mays]

Seq. No. 399509
 Seq. ID LIB3431-025-P1-K1-F2
 Method BLASTX
 NCBI GI g132105
 BLAST score 423
 E value 2.0e-41
 Match length 81
 % identity 96
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 399510
 Seq. ID LIB3431-025-P1-K1-F3
 Method BLASTX
 NCBI GI g4467098
 BLAST score 324
 E value 1.0e-29
 Match length 136
 % identity 44
 NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 399511
 Seq. ID LIB3431-025-P1-K1-F5
 Method BLASTX
 NCBI GI g6093671
 BLAST score 388
 E value 2.0e-37
 Match length 122
 % identity 61
 NCBI Description CATIONIC PEROXIDASE 1 PRECURSOR >gi_1491776 (M37636) cationic peroxidase [Arachis hypogaea]

Seq. No. 399512
 Seq. ID LIB3431-025-P1-K1-F6
 Method BLASTX

NCBI GI g1617197
 BLAST score 304
 E value 2.0e-27
 Match length 76
 % identity 76
 NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 399513
 Seq. ID LIB3431-025-P1-K1-F7
 Method BLASTX
 NCBI GI g4938484
 BLAST score 326
 E value 6.0e-30
 Match length 205
 % identity 45
 NCBI Description (AL078464) transcription factor-like protein [Arabidopsis thaliana]

Seq. No. 399514
 Seq. ID LIB3431-025-P1-K1-F8
 Method BLASTX
 NCBI GI g1706260
 BLAST score 355
 E value 2.0e-33
 Match length 68
 % identity 94
 NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir_S59597
 cysteine proteinase 1 precursor - maize
 >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea mays]

Seq. No. 399515
 Seq. ID LIB3431-025-P1-K1-F9
 Method BLASTX
 NCBI GI g5815410
 BLAST score 828
 E value 4.0e-94
 Match length 209
 % identity 83
 NCBI Description (AF177392) blast and wounding induced mitogen-activated protein kinase [Oryza sativa]

Seq. No. 399516
 Seq. ID LIB3431-025-P1-K1-G10
 Method BLASTX
 NCBI GI g1653953
 BLAST score 212
 E value 6.0e-17
 Match length 130
 % identity 38
 NCBI Description (D90917) hypothetical protein [Synechocystis sp.]

Seq. No. 399517
 Seq. ID LIB3431-025-P1-K1-G9
 Method BLASTX
 NCBI GI g3789954
 BLAST score 1065

E value 1.0e-116
 Match length 199
 % identity 100
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 399518
 Seq. ID LIB3431-025-P1-K1-H10
 Method BLASTX
 NCBI GI g1737492
 BLAST score 626
 E value 4.0e-65
 Match length 177
 % identity 71
 NCBI Description (U81318) poly(A)-binding protein [Triticum aestivum]

Seq. No. 399519
 Seq. ID LIB3431-025-P1-K1-H3
 Method BLASTX
 NCBI GI g3913641
 BLAST score 1185
 E value 1.0e-130
 Match length 227
 % identity 100
 NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_3041777_dbj_BAA25423_ (AB007194) fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No. 399520
 Seq. ID LIB3431-025-P1-K1-H4
 Method BLASTX
 NCBI GI g4678280
 BLAST score 259
 E value 5.0e-22
 Match length 152
 % identity 36
 NCBI Description (AL049660) zinc finger-like protein [Arabidopsis thaliana]

Seq. No. 399521
 Seq. ID LIB3431-025-P1-K1-H7
 Method BLASTX
 NCBI GI g115787
 BLAST score 544
 E value 1.0e-107
 Match length 224
 % identity 91
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 399522
 Seq. ID LIB3431-025-P1-K1-H9
 Method BLASTX
 NCBI GI g3036951

BLAST score 611
 E value 2.0e-63
 Match length 117
 % identity 98
 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 399523
 Seq. ID LIB3431-025-P1-N1-A1
 Method BLASTX
 NCBI GI g3885882
 BLAST score 275
 E value 3.0e-24
 Match length 55
 % identity 98
 NCBI Description (AF093629) inorganic pyrophosphatase [Oryza sativa]

Seq. No. 399524
 Seq. ID LIB3431-025-P1-N1-A11
 Method BLASTX
 NCBI GI g3808101
 BLAST score 303
 E value 1.0e-27
 Match length 73
 % identity 88
 NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]

Seq. No. 399525
 Seq. ID LIB3431-025-P1-N1-A12
 Method BLASTN
 NCBI GI g2072554
 BLAST score 330
 E value 0.0e+00
 Match length 330
 % identity 100
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 399526
 Seq. ID LIB3431-025-P1-N1-A5
 Method BLASTN
 NCBI GI g395929
 BLAST score 82
 E value 5.0e-38
 Match length 145
 % identity 90
 NCBI Description O.sativa retrotransposon Tos1-1

Seq. No. 399527
 Seq. ID LIB3431-025-P1-N1-A7
 Method BLASTX
 NCBI GI g693920
 BLAST score 340
 E value 6.0e-32
 Match length 68
 % identity 96
 NCBI Description (U21113) chlorophyll a/b binding protein [Solanum

Seq. No. 399533
 Seq. ID LIB3431-025-P1-N1-B3
 Method BLASTN
 NCBI GI g433216
 BLAST score 211
 E value 1.0e-115
 Match length 232
 % identity 97
 NCBI Description Rice mRNA for ascorbate peroxidase (gene name SS622), partial cds

Seq. No. 399534
 Seq. ID LIB3431-025-P1-N1-B8
 Method BLASTX
 NCBI GI g1617197
 BLAST score 300
 E value 3.0e-27
 Match length 71
 % identity 77
 NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 399535
 Seq. ID LIB3431-025-P1-N1-B9
 Method BLASTX
 NCBI GI g729135
 BLAST score 267
 E value 2.0e-23
 Match length 55
 % identity 89
 NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYL-L-METHIONINE:CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir_S28612 catechol O-methyltransferase (EC 2.1.1.6) - maize >gi_168532 (M73235) O-methyltransferase [Zea mays]

Seq. No. 399536
 Seq. ID LIB3431-025-P1-N1-C11
 Method BLASTX
 NCBI GI g129707
 BLAST score 405
 E value 2.0e-39
 Match length 97
 % identity 84
 NCBI Description PROTOCHLOROPHYLLIDE REDUCTASE (PCR) (NADPH-PROTOCHLOROPHYLLIDE OXIDOREDUCTASE) >gi_100550_pir_S08406 protochlorophyllide reductase (EC 1.3.1.33) - oat (fragment) >gi_829253_emb_CAA34913 (X17067) protochlorophyllide reductase (314 AA) [Avena sativa]

Seq. No. 399537
 Seq. ID LIB3431-025-P1-N1-C4
 Method BLASTX
 NCBI GI g3126854
 BLAST score 523
 E value 3.0e-53
 Match length 99

09684016-101000

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% identity          99
NCBI Description    (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.            399538
Seq. ID             LIB3431-025-P1-N1-C6
Method              BLASTX
NCBI GI             g2072555
BLAST score         228
E value             1.0e-18
Match length        42
% identity          100
NCBI Description    (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
protein [Oryza sativa]

Seq. No.            399539
Seq. ID             LIB3431-025-P1-N1-C7
Method              BLASTX
NCBI GI             g3914466
BLAST score         395
E value             2.0e-38
Match length        72
% identity          99
NCBI Description    PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
(PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN
subunit precursor [Zea mays]

Seq. No.            399540
Seq. ID             LIB3431-025-P1-N1-C9
Method              BLASTX
NCBI GI             g517500
BLAST score         374
E value             7.0e-36
Match length        90
% identity          81
NCBI Description    (M87435) precursor of the oxygen evolving complex 17 kDa
protein [Zea mays] >gi_444338_prf__1906386A photosystem II
OE17 protein [Pisum sativum]

Seq. No.            399541
Seq. ID             LIB3431-025-P1-N1-D1
Method              BLASTX
NCBI GI             g1353352
BLAST score         227
E value             1.0e-18
Match length        59
% identity          75
NCBI Description    (U31975) alanine aminotransferase [Chlamydomonas
reinhardtii]

Seq. No.            399542
Seq. ID             LIB3431-025-P1-N1-D10
Method              BLASTX
NCBI GI             g3126854
BLAST score         392
E value             5.0e-38
Match length        74

```

% identity 100
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 399543
 Seq. ID LIB3431-025-P1-N1-D11
 Method BLASTX
 NCBI GI g5091556
 BLAST score 194
 E value 9.0e-15
 Match length 55
 % identity 58
 NCBI Description (AC007067) T10024.25 [Arabidopsis thaliana]

Seq. No. 399544
 Seq. ID LIB3431-025-P1-N1-D12
 Method BLASTX
 NCBI GI g1841466
 BLAST score 182
 E value 2.0e-13
 Match length 32
 % identity 94
 NCBI Description (Y11003) putative pre-pro-cysteine proteinase [Nicotiana tabacum]

Seq. No. 399545
 Seq. ID LIB3431-025-P1-N1-D2
 Method BLASTX
 NCBI GI g4587990
 BLAST score 250
 E value 2.0e-21
 Match length 88
 % identity 50
 NCBI Description (AF085279) hypothetical protein [Arabidopsis thaliana]

Seq. No. 399546
 Seq. ID LIB3431-025-P1-N1-D4
 Method BLASTX
 NCBI GI g2598151
 BLAST score 222
 E value 5.0e-18
 Match length 43
 % identity 95
 NCBI Description (AF027350) NADPH:protochlorophyllide oxidoreductase porB [Pinus taeda]

Seq. No. 399547
 Seq. ID LIB3431-025-P1-N1-D7
 Method BLASTX
 NCBI GI g417260
 BLAST score 300
 E value 3.0e-27
 Match length 76
 % identity 75
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

sativa]

Seq. No. 399553
 Seq. ID LIB3431-025-P1-N1-E6
 Method BLASTN
 NCBI GI g5777612
 BLAST score 407
 E value 0.0e+00
 Match length 418
 % identity 99
 NCBI Description Oryza sativa chromosome 4 BAC q3037-207F1 complete genome

Seq. No. 399554
 Seq. ID LIB3431-025-P1-N1-E7
 Method BLASTN
 NCBI GI g1841354
 BLAST score 66
 E value 2.0e-29
 Match length 66
 % identity 100
 NCBI Description Oryza sativa mitochondrial DNA for cytochrome c oxidase subunit Vb precursor, complete cds

Seq. No. 399555
 Seq. ID LIB3431-025-P1-N1-E8
 Method BLASTX
 NCBI GI g3036951
 BLAST score 427
 E value 4.0e-42
 Match length 80
 % identity 100
 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana glauca]

Seq. No. 399556
 Seq. ID LIB3431-025-P1-N1-E9
 Method BLASTX
 NCBI GI g3913239
 BLAST score 256
 E value 4.0e-40
 Match length 132
 % identity 75
 NCBI Description PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE (DXP SYNTHASE) >gi_2612941 (AF024512) CLA1 transketolase-like protein [Oryza sativa]

Seq. No. 399557
 Seq. ID LIB3431-025-P1-N1-F10
 Method BLASTN
 NCBI GI g600766
 BLAST score 296
 E value 1.0e-166
 Match length 364
 % identity 95
 NCBI Description Oryza sativa cyclophilin 2 (Cyp2) gene, complete cds

Seq. No. 399558

Seq. ID LIB3431-025-P1-N1-F11
 Method BLASTX
 NCBI GI g1777961
 BLAST score 342
 E value 4.0e-32
 Match length 114
 % identity 61
 NCBI Description (U56406) methyljasmonate-inducible lipxygenase 2 [Hordeum vulgare]

Seq. No. 399559
 Seq. ID LIB3431-025-P1-N1-F2
 Method BLASTX
 NCBI GI g347451
 BLAST score 236
 E value 1.0e-19
 Match length 47
 % identity 98
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 399560
 Seq. ID LIB3431-025-P1-N1-F5
 Method BLASTX
 NCBI GI g520568
 BLAST score 262
 E value 1.0e-22
 Match length 87
 % identity 63
 NCBI Description (U12314) peroxidase [Cenchrus ciliaris]

Seq. No. 399561
 Seq. ID LIB3431-025-P1-N1-F6
 Method BLASTX
 NCBI GI g1617197
 BLAST score 287
 E value 1.0e-25
 Match length 71
 % identity 73
 NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 399562
 Seq. ID LIB3431-025-P1-N1-F8
 Method BLASTX
 NCBI GI g2118130
 BLAST score 255
 E value 7.0e-22
 Match length 47
 % identity 94
 NCBI Description cysteine proteinase (EC 3.4.22.-), glucose starvation-induced - maize (fragment)
 >gi_559532_emb_CAA57675_ (X82185) cysteine proteinase [Zea mays]

Seq. No. 399563
 Seq. ID LIB3431-025-P1-N1-F9
 Method BLASTN

NCBI GI g5815409
 BLAST score 420
 E value 0.0e+00
 Match length 449
 % identity 98
 NCBI Description Oryza sativa blast and wounding induced mitogen-activated protein kinase (BWMK1) mRNA, complete cds

Seq. No. 399564
 Seq. ID LIB3431-025-P1-N1-G10
 Method BLASTX
 NCBI GI g1653953
 BLAST score 190
 E value 3.0e-14
 Match length 91
 % identity 42
 NCBI Description (D90917) hypothetical protein [Synechocystis sp.]

Seq. No. 399565
 Seq. ID LIB3431-025-P1-N1-G11
 Method BLASTX
 NCBI GI g2130073
 BLAST score 308
 E value 4.0e-28
 Match length 60
 % identity 100
 NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301) aldolase C-1 [Oryza sativa]

Seq. No. 399566
 Seq. ID LIB3431-025-P1-N1-G12
 Method BLASTN
 NCBI GI g786177
 BLAST score 55
 E value 4.0e-22
 Match length 130
 % identity 86
 NCBI Description Rice DNA for aldolase C-1, complete cds

Seq. No. 399567
 Seq. ID LIB3431-025-P1-N1-G3
 Method BLASTX
 NCBI GI g2708745
 BLAST score 197
 E value 3.0e-15
 Match length 48
 % identity 81
 NCBI Description (AC003952) putative calcium-dependent ser/thr protein kinase [Arabidopsis thaliana]

Seq. No. 399568
 Seq. ID LIB3431-025-P1-N1-G5
 Method BLASTX
 NCBI GI g21839
 BLAST score 229

E value 7.0e-19
 Match length 47
 % identity 96
 NCBI Description (X57952) phosphoribulokinase [*Triticum aestivum*]

Seq. No. 399569
 Seq. ID LIB3431-025-P1-N1-G9
 Method BLASTX
 NCBI GI g3789954
 BLAST score 354
 E value 2.0e-33
 Match length 66
 % identity 98
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [*Oryza sativa*]

Seq. No. 399570
 Seq. ID LIB3431-025-P1-N1-H10
 Method BLASTX
 NCBI GI g1737492
 BLAST score 280
 E value 6.0e-25
 Match length 70
 % identity 80
 NCBI Description (U81318) poly(A)-binding protein [*Triticum aestivum*]

Seq. No. 399571
 Seq. ID LIB3431-025-P1-N1-H12
 Method BLASTX
 NCBI GI g517500
 BLAST score 296
 E value 8.0e-27
 Match length 94
 % identity 67
 NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa protein [*Zea mays*] >gi_444338_prf__1906386A photosystem II OE17 protein [*Pisum sativum*]

Seq. No. 399572
 Seq. ID LIB3431-025-P1-N1-H2
 Method BLASTX
 NCBI GI g1651922
 BLAST score 176
 E value 1.0e-12
 Match length 59
 % identity 56
 NCBI Description (D90901) hypothetical protein [*Synechocystis* sp.]

Seq. No. 399573
 Seq. ID LIB3431-025-P1-N1-H3
 Method BLASTX
 NCBI GI g3913641
 BLAST score 529
 E value 5.0e-54
 Match length 100
 % identity 100
 NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR

```
(D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
>gi_3041777_dbj_BAA25423_ (AB007194)
fructose-1,6-bisphosphatase [Oryza sativa]
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```
Seq. No.      399574
Seq. ID      LIB3431-025-P1-N1-H5
Method       BLASTX
NCBI GI      g129707
BLAST score   419
E value      4.0e-41
Match length  95
% identity    86
NCBI Description  PROTOCHLOROPHYLLIDE REDUCTASE (PCR)
                  (NADPH-PROTOCHLOROPHYLLIDE OXIDOREDUCTASE)
                  >gi_100550_pir_S08406 protochlorophyllide reductase (EC
                  1.3.1.33) - oat (fragment) >gi_829253_emb_CAA34913_
                  (X17067) protochlorophyllide reductase (314 AA) [Avena
                  sativa]
```

Seq. No.	399575
Seq. ID	LIB3431-025-P1-N1-H7
Method	BLASTX
NCBI GI	g4512125
BLAST score	243
E value	1.0e-20
Match length	45
% identity	100
NCBI Description	(AF133340) putative chlorophyll a/b-binding protein [Phalaenopsis sp. 'KCbutterfly']

```
Seq. No.          399576
Seq. ID           LIB3431-025-P1-N1-H8
Method            BLASTX
NCBI GI           g267120
BLAST score       284
E value           2.0e-25
Match length      71
% identity        77
NCBI Description   THIOREDOXIN F-TYPE, CHLOROPLAST PRECURSOR (TRX-F)
                  >gi_100070_pir_S20929 thioredoxin f precursor - garden pea
                  >gi_20907_emb_CAA45098_(X63537) thioredoxin F [Pisum
                  sativum] >gi_1388086 (U35830) thioredoxin f [Pisum sativum]
```

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Seq. No.      399577
Seq. ID      LIB3431-025-P1-N1-H9
Method       BLASTX
NCBI GI      g3036951
BLAST score   450
E value      9.0e-45
Match length  85
% identity    100
NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein
[Nicotiana glauca]
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Seq. No.      399578
Seq. ID      LIB3431-026-P1-K1-A1
Method       BLASTX
```


E value 8.0e-39
 Match length 98
 % identity 77
 NCBI Description IN2-2 PROTEIN

Seq. No. 399584
 Seq. ID LIB3431-026-P1-K1-A4
 Method BLASTX
 NCBI GI g132105
 BLAST score 672
 E value 7.0e-71
 Match length 124
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 399585
 Seq. ID LIB3431-026-P1-K1-A5
 Method BLASTX
 NCBI GI g3345477
 BLAST score 269
 E value 1.0e-23
 Match length 98
 % identity 58
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 399586
 Seq. ID LIB3431-026-P1-K1-A6
 Method BLASTX
 NCBI GI g4538920
 BLAST score 150
 E value 1.0e-09
 Match length 57
 % identity 60
 NCBI Description (AL049483) nitrogen fixation like protein [Arabidopsis
 thaliana]

Seq. No. 399587
 Seq. ID LIB3431-026-P1-K1-A7
 Method BLASTN
 NCBI GI g218209
 BLAST score 34
 E value 1.0e-09
 Match length 78
 % identity 87
 NCBI Description Oryza sativa mRNA for the small subunit of
 ribulose-1,5-bisphosphate carboxylase, complete cds, clone
 pOSSS2106

Seq. No. 399588

Method BLASTX
 NCBI GI g3868756
 BLAST score 494
 E value 3.0e-50
 Match length 88
 % identity 100
 NCBI Description (D86611) catalase [Oryza sativa]

Seq. No. 399599
 Seq. ID LIB3431-026-P1-K1-C1
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 399600
 Seq. ID LIB3431-026-P1-K1-C10
 Method BLASTX
 NCBI GI g5668640
 BLAST score 515
 E value 2.0e-52
 Match length 148
 % identity 61
 NCBI Description (AL109619) putative protein [Arabidopsis thaliana]

Seq. No. 399601
 Seq. ID LIB3431-026-P1-K1-C3
 Method BLASTX
 NCBI GI g132105
 BLAST score 713
 E value 2.0e-75
 Match length 131
 % identity 99
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone POSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 399602
 Seq. ID LIB3431-026-P1-K1-C4
 Method BLASTX
 NCBI GI g125580
 BLAST score 498
 E value 2.0e-50
 Match length 116
 % identity 85
 NCBI Description PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)

00684015.101000

>gi_871510_emb_CAA90080_ (Z49900) small GTP-binding protein
[Pisum sativum]

Seq. No. 399608
Seq. ID LIB3431-026-P1-K1-D10
Method BLASTX
NCBI GI g115787
BLAST score 489
E value 2.0e-49
Match length 113
% identity 87
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 399609
Seq. ID LIB3431-026-P1-K1-D11
Method BLASTX
NCBI GI g2688839
BLAST score 531
E value 3.0e-54
Match length 136
% identity 69
NCBI Description (AF003347) ATP phosphoribosyltransferase [Thlaspi goesingense]

Seq. No. 399610
Seq. ID LIB3431-026-P1-K1-D12
Method BLASTX
NCBI GI g3176690
BLAST score 639
E value 6.0e-67
Match length 129
% identity 91
NCBI Description (AC003671) Similar to ubiquitin ligase gb_D63905 from S. cerevisiae. EST gb_R65295 comes from this gene. [Arabidopsis thaliana]

Seq. No. 399611
Seq. ID LIB3431-026-P1-K1-D4
Method BLASTX
NCBI GI g3004565
BLAST score 289
E value 8.0e-29
Match length 80
% identity 79
NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 399612
Seq. ID LIB3431-026-P1-K1-D5
Method BLASTX
NCBI GI g320618
BLAST score 558
E value 2.0e-57
Match length 124

Seq. ID LIB3431-026-P1-K1-F11
 Method BLASTX
 NCBI GI g115796
 BLAST score 848
 E value 2.0e-91
 Match length 159
 % identity 98
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi_218174_dbj_BAA00537_ (D00642) type II light-harvesting chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 399624
 Seq. ID LIB3431-026-P1-K1-F12
 Method BLASTX
 NCBI GI g131388
 BLAST score 257
 E value 3.0e-22
 Match length 102
 % identity 61
 NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir_S16260 photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum aestivum]

Seq. No. 399625
 Seq. ID LIB3431-026-P1-K1-F2
 Method BLASTX
 NCBI GI g2407281
 BLAST score 632
 E value 3.0e-66
 Match length 116
 % identity 99
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 399626
 Seq. ID LIB3431-026-P1-K1-F4
 Method BLASTX
 NCBI GI g132105
 BLAST score 567
 E value 2.0e-58
 Match length 122
 % identity 87
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Method	BLASTX
NCBI GI	g129915
BLAST score	492
E value	8.0e-50
Match length	104
% identity	92
NCBI Description	PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR >gi_66912_pir_TVWTGC phosphoglycerate kinase (EC 2.7.2.3) precursor, chloroplast - wheat >gi_21833_emb_CAA33303 (X15233) phosphoglycerate kinase (AA 1 - 480) [Triticum aestivum] >gi_3293043_emb_CAA51931 (X73528) phosphoglycerate kinase [Triticum aestivum]
Seq. No.	399638
Seq. ID	LIB3431-026-P1-K1-G9
Method	BLASTX
NCBI GI	g131176
BLAST score	299
E value	5.0e-27
Match length	58
% identity	98
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E) >gi_72683_pir_F1BH4 photosystem I chain IV precursor - barley >gi_19087_emb_CAA68782 (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf_1413233A 10.8kD photosystem I protein [Hordeum vulgare var. distichum]
Seq. No.	399639
Seq. ID	LIB3431-026-P1-K1-H11
Method	BLASTX
NCBI GI	g3292814
BLAST score	298
E value	7.0e-27
Match length	80
% identity	68
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]
Seq. No.	399640
Seq. ID	LIB3431-026-P1-K1-H3
Method	BLASTX
NCBI GI	g3411227
BLAST score	402
E value	3.0e-39
Match length	84
% identity	90
NCBI Description	(AF078874) NBS-LRR type disease resistance protein O2 [Avena sativa]
Seq. No.	399641
Seq. ID	LIB3431-026-P1-K1-H4
Method	BLASTX
NCBI GI	g3913018
BLAST score	694
E value	2.0e-73
Match length	140

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Seq. No.      399651
Seq. ID      LIB3431-026-P1-N1-A3
Method       BLASTX
NCBI GI      g2462750
BLAST score   240
E value      4.0e-20
```

```
Match length      65
% identity        69
NCBI Description  (AC002292) Highly similar to auxin-induced protein
                  (aldo/keto reductase family) [Arabidopsis thaliana]
```

```
Seq. No.      399652
Seq. ID      LIB3431-026-P1-N1-A4
Method       BLASTX
NCBI GI      g132105
BLAST score   277
E value      2.0e-24
Match length  53
% identity    100
NCBI Description  RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
```

```
Seq. No.      399653
Seq. ID      LIB3431-026-P1-N1-A5
Method       BLASTX
NCBI GI      g3345477
BLAST score   210
E value      1.0e-16
Match length  40
% identity    97
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
```

```
Seq. No.      399654
Seq. ID      LIB3431-026-P1-N1-A6
Method       BLASTX
NCBI GI      g4538920
BLAST score   226
E value      2.0e-18
Match length  59
% identity   81
NCBI Description (AL049483) nitrogen fixation like protein [Arabidopsis thaliana]
```

```
Seq. No.      399655
Seq. ID      LIB3431-026-P1-N1-A7
Method       BLASTX
NCBI GI      g3913437
BLAST score   196
E value      2.0e-15
Match length  41
% identity    85
NCBI Description  PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
                HELICASE >gi_1402875_emb_CAA66825_ (X98130) RNA helicase
                [Arabidopsis thaliana] >gi_1495271_emb_CAA66613_ (X97970)
                RNA helicase [Arabidopsis thaliana]
```

09634076 3103000

09694076 3103000

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000T0T" 9T04B960

Seq. No. 399661
 Seq. ID LIB3431-026-P1-N1-B2
 Method BLASTN
 NCBI GI g5478796
 BLAST score 349
 E value 0.0e+00
 Match length 431
 % identity 100
 NCBI Description Oryza sativa CAO mRNA for chlorophyll b synthase, partial cds

Seq. No. 399662
 Seq. ID LIB3431-026-P1-N1-B3
 Method BLASTX
 NCBI GI g1173347
 BLAST score 250
 E value 2.0e-21
 Match length 54
 % identity 94
 NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507 (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]

Seq. No. 399663
 Seq. ID LIB3431-026-P1-N1-B4
 Method BLASTX
 NCBI GI g1835731
 BLAST score 359
 E value 4.0e-34
 Match length 80
 % identity 88
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 399664
 Seq. ID LIB3431-026-P1-N1-B5
 Method BLASTX
 NCBI GI g1835731
 BLAST score 359
 E value 4.0e-34
 Match length 80
 % identity 88
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 399665
 Seq. ID LIB3431-026-P1-N1-B6
 Method BLASTX
 NCBI GI g3929924
 BLAST score 292
 E value 3.0e-26
 Match length 56
 % identity 98
 NCBI Description (AB020502) catalase [Oryza sativa]

Seq. No. 399666
 Seq. ID LIB3431-026-P1-N1-B8
 Method BLASTX
 NCBI GI g517500
 BLAST score 401
 E value 4.0e-39
 Match length 97
 % identity 81
 NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf__1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No. 399667
 Seq. ID LIB3431-026-P1-N1-C1
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 399668
 Seq. ID LIB3431-026-P1-N1-C10
 Method BLASTX
 NCBI GI g5668640
 BLAST score 332
 E value 6.0e-31
 Match length 97
 % identity 57
 NCBI Description (AL109619) putative protein [Arabidopsis thaliana]

Seq. No. 399669
 Seq. ID LIB3431-026-P1-N1-C12
 Method BLASTX
 NCBI GI g4455296
 BLAST score 241
 E value 3.0e-20
 Match length 44
 % identity 89
 NCBI Description (AL035528) hypothetical protein [Arabidopsis thaliana]

Seq. No. 399670
 Seq. ID LIB3431-026-P1-N1-C3
 Method BLASTX
 NCBI GI g132105
 BLAST score 301
 E value 3.0e-27
 Match length 57
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate

[Phalaenopsis sp. 'KCbutterfly']

Seq. No. 399676
Seq. ID LIB3431-026-P1-N1-D3
Method BLASTX
NCBI GI g120661
BLAST score 181
E value 3.0e-13
Match length 45
% identity 76
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST
PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate
dehydrogenase A-subunit precursor [Nicotiana tabacum]

Seq. No. 399677
Seq. ID LIB3431-026-P1-N1-D4
Method BLASTX
NCBI GI g3004565
BLAST score 337
E value 2.0e-31
Match length 94
% identity 67
NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 399678
Seq. ID LIB3431-026-P1-N1-D5
Method BLASTX
NCBI GI g115787
BLAST score 409
E value 6.0e-40
Match length 77
% identity 100
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
protein 2R precursor - rice >gi_20182_emb_CAA32109
(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
[Oryza sativa]

Seq. No. 399679
Seq. ID LIB3431-026-P1-N1-D6
Method BLASTX
NCBI GI g543939
BLAST score 160
E value 9.0e-11
Match length 39
% identity 85
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN CP24 PRECURSOR
>gi_541819_pir_S40210 chlorophyll a/b-binding protein CP24
precursor - spinach >gi_437991_emb_CAA81105.1 (Z25886) 20
kDa protein of CP24 precursor protein [Spinacia oleracea]

Seq. No. 399680
Seq. ID LIB3431-026-P1-N1-D8
Method BLASTX
NCBI GI g170131
BLAST score 218
E value 1.0e-17


```
Seq. No.      399695
Seq. ID      LIB3431-026-P1-N1-G2
Method       BLASTX
NCBI GI      g1076724
BLAST score   364
E value      1.0e-34
Match length  70
% identity    94
NCBI Description
LHCI-680, photosystem I antenna protein - barley
>gi_666054_emb_CAA59049_(X84308) LHCI-680, photosystem I
antenna protein [Hordeum vulgare]
```

Seq. No.	399696
Seq. ID	LIB3431-026-P1-N1-G4
Method	BLASTN
NCBI GI	g3885887
BLAST score	423
E value	0.0e+00
Match length	423
% identity	100
NCBI Description	Oryza sativa high mobility group protein (HMG) mRNA, complete cds

```
Seq. No.          399697
Seq. ID           LIB3431-026-P1-N1-G5
Method            BLASTN
NCBI GI           g2306980
BLAST score       112
E value           2.0e-56
Match length      125
% identity        98
NCBI Description   Oryza sativa photosystem I antenna protein (Lhca) mRNA,
                   complete cds
```

Seq. No.	399698
Seq. ID	LIB3431-026-P1-N1-G6
Method	BLASTX
NCBI GI	g2130089
BLAST score	222
E value	5.0e-18
Match length	42
% identity	93
NCBI Description	2-oxoglutarate/malate translocator (clone OMT103), mitochondrial membrane - proso millet >gi_1100743_dbj_BAA08105_ (D45075) 2-oxoglutarate/malate translocator [Panicum miliaceum]

```
Seq. No.      399699
Seq. ID      LIB3431-026-P1-N1-G7
Method       BLASTX
NCBI GI      g3036946
BLAST score   300
E value      3.0e-27
Match length  57
% identity    100
NCBI Description (AB012637) light harvesting chlorophyll a/b-binding protein
```

0694-0167

```
Seq. No.      399701
Seq. ID      LIB3431-026-P1-N1-G9
Method       BLASTX
NCBI GI      g1311176
BLAST score   187
E value      6.0e-14
Match length  37
% identity    97
NCBI Description  PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR
                  (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
                  >gi_72683_pir_F1BH4 photosystem I chain IV precursor -
                  barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA
                  -46 to 101) [Hordeum vulgare] >gi_226163_prf_1413233A
                  10.8kD photosystem I protein [Hordeum vulgare var.
                  distichum]
```

```
Seq. No.      399702
Seq. ID      LIB3431-026-P1-N1-H11
Method       BLASTX
NCBI GI      g3292814
BLAST score   232
E value      3.0e-19
Match length  57
% identity    72
NCBI Description (AL031018) putative protein [Arabidopsis thaliana]
```

```
Seq. No.      399703
Seq. ID      LIB3431-026-P1-N1-H3
Method       BLASTX
NCBI GI      g4490715
BLAST score   147
E value      3.0e-09
Match length  99
% identity    34
NCBI Description (AL035680) putative protein [Arabidopsis thaliana]
```

51130


```
Seq. No.      399709
Seq. ID      LIB3431-027-P1-K1-A11
Method       BLASTX
NCBI GI      g4557229
BLAST score   223
E value      4.0e-18
Match length  112
% identity    35
NCBI Description  angio-associated, migratory cell protein
                  >gi_3121739_sp_Q13685 AAMP HUMAN ANGIO-ASSOCIATED MIGRATORY
                  CELL PROTEIN >gi_2134759_pir_I39383 angio-associated
                  migratory cell protein - human >gi_870803 (M95627)
                  angio-associated migratory cell protein [Homo sapiens]
```

```
Seq. No.      399710
Seq. ID       LIB3431-027-P1-K1-A12
Method        BLASTX
NCBI GI       g2493650
BLAST score   638
E value       7.0e-67
Match length  139
% identity    95
NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD
                  CHAPERONIN BETA SUBUNIT) (CPN-60 BETA)
                  >gi_1167858_emb_CAA93139_ (Z68903) chaperonin [Secale
                  cereale]
```

```

Seq. No.      399711
Seq. ID       LIB3431-027-P1-K1-A3
Method        BLASTX
NCBI GI       g417103
BLAST score   541
E value       2.0e-55
Match length  124
% identity    88
NCBI Description HISTONE H3.2, MINOR >gi_282871_pir_S24346 histone
H3.3-like protein - Arabidopsis thaliana
>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi_488563
(U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460)
histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone
H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2
[Medicago sativa] >gi_488577 (U09465) histone H3.2
[Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone
H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422)
histone H3 variant H3.3 [Lycopersicon esculentum]
>gi_2558944 (AF024716) histone 3 [Gossypium hirsutum]
>gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana
tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa]
>gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia
coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone
H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_
(AL035708) Histone H3 [Arabidopsis thaliana]
>gi_6006364_dbj_BAA84794.1_ (AP000559) EST D15300(C0425)
corresponds to a region of the predicted gene.; Similar to

```

09634-0167

```
Seq. No.          399713
Seq. ID           LIB3431-027-P1-K1-A5
Method            BLASTX
NCBI GI           g2388689
BLAST score       270
E value           1.0e-23
Match length      67
% identity        76
NCBI Description  (AF016633) GH1 protein [Glycine max]
```

```
Seq. No.      399715
Seq. ID      LIB3431-027-P1-K1-A7
Method       BLASTX
NCBI GI      g1173347
BLAST score   802
E value      5.0e-86
Match length  153
% identity    95
NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC
                3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                aestivum]
```

51133

05084016 101000

```
Seq. No.      399726
Seq. ID      LIB3431-027-P1-K1-C10
Method       BLASTX
NCBI GI      g1707998
BLAST score   297
E value      9.0e-27
Match length  92
% identity    66
NCBI Description SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR
                (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                (SHMT) >gi_481944_pir_S40218 glycine
                hydroxymethyltransferase (EC 2.1.2.1) - potato
                >gi_438247_emb_CAA81082_ (Z25863) glycine
                hydroxymethyltransferase [Solanum tuberosum]
```

```
Seq. No.      399727
Seq. ID      LIB3431-027-P1-K1-C11
Method       BLASTX
NCBI GI      g3482977
BLAST score   273
E value      5.0e-24
Match length  138
% identity    46
NCBI Description (AL031369) putative protein [Arabidopsis thaliana]
```

```
Seq. No.      399728
Seq. ID      LIB3431-027-P1-K1-C12
Method       BLASTX
NCBI GI      g100796
BLAST score   752
E value      4.0e-80
Match length  152
% identity    94
NCBI Description  phosphoribulokinase (EC 2.7.1.19) - wheat
```

51136

000101-91013950

Match length 118
% identity 68
NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
>gi_226872_prf_1609235A chlorophyll a/b binding protein
[Lycopersicon esculentum]

Seq. No. 399730
Seq. ID LIB3431-027-P1-K1-C4
Method BLASTX
NCBI GI g1669341
BLAST score 219
E value 1.0e-17
Match length 133
% identity 41
NCBI Description (D45066) AOBP (ascorbate oxidase promoter-binding protein)
[Cucurbita maxima]

Seq. No. 399731
Seq. ID LIB3431-027-P1-K1-C5
Method BLASTX
NCBI GI g4585882
BLAST score 498
E value 2.0e-50
Match length 150
% identity 64
NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein
[Arabidopsis thaliana]

Seq. No. 399732
Seq. ID LIB3431-027-P1-K1-C6
Method BLASTX
NCBI GI g5922612
BLAST score 282
E value 5.0e-25
Match length 127
% identity 46
NCBI Description (AP000492) EST AU078118(E3904) corresponds to a region of
the predicted gene.; similar to Arabidopsis thaliana BAC
IG002P16; No definition line found. (AF007270) [Oryza
sativa]

Seq. No. 399733
Seq. ID LIB3431-027-P1-K1-C9
Method BLASTX
NCBI GI g671740
BLAST score 219
E value 1.0e-17
Match length 48
% identity 88
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
construct]

Seq. No. 399734
Seq. ID LIB3431-027-P1-K1-D1
Method BLASTX
NCBI GI g2244926
BLAST score 292


```
Seq. No.      399745
Seq. ID      LIB3431-027-P1-K1-E6
Method       BLASTX
NCBI GI      g5354158
BLAST score   384
E value      3.0e-43
Match length  140
% identity    64
NCBI Description (AF149841) digalactosyldiacylglycerol synthase [Arabidopsis
thaliana] >gi_5354160_gb_AAD42379.1_AF149842_1 (AF149842)
digalactosyldiacylglycerol synthase [Arabidopsis thaliana]
>gi_6041825_gb_AAF02140.1_AC009918_12 (AC009918)
digalactosyldiacylglycerol synthase [Arabidopsis thaliana]
```

```
Seq. No.          399746
Seq. ID           LIB3431-027-P1-K1-E7
Method            BLASTX
NCBI GI           g729668
BLAST score       241
E value           3.0e-20
Match length      68
% identity        63
NCBI Description   HISTONE H1 >gi_2147479_pir_S65059 histone H1,
                   drought-inducible - Lycopersicon pennellii >gi_436823
                   (U01890). Solanum pennellii histone H1 [Solanum pennellii]
```

```
Seq. No.      399747
Seq. ID      LIB3431-027-P1-K1-E8
Method       BLASTX
NCBI GI      g1835731
BLAST score   412
E value      3.0e-40
Match length  89
% identity    88
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
```

```
Seq. No.      399748
Seq. ID      LIB3431-027-P1-K1-E9
Method       BLASTX
NCBI GI      g3885894
BLAST score   464
E value      2.0e-46
Match length  110
% identity    82
NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
```

```
Seq. No.          399749
Seq. ID           LIB3431-027-P1-K1-F1
Method            BLASTX
NCBI GI           g1076722
BLAST score       667
E value           4.0e-70
Match length      144
% identity        90
NCBI Description   hypothetical protein - barley (fragment)
```

Seq. No.	399750
Seq. ID	LIB3431-027-P1-K1-F10
Method	BLASTX
NCBI GI	g1777961
BLAST score	504
E value	5.0e-51
Match length	154
% identity	58
NCBI Description	(U56406) methyljasmonate-inducible lipoxygenase 2 [Hordeum vulgare]

```
Seq. No.      399751
Seq. ID      LIB3431-027-P1-K1-F11
Method       BLASTX
NCBI GI      g2072555
BLAST score   237
E value      9.0e-20
Match length  44
% identity    100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
protein [Oryza sativa]
```

```
Seq. No.      399752
Seq. ID      LIB3431-027-P1-K1-F12
Method       BLASTX
NCBI GI      g3510256
BLAST score   157
E value      2.0e-10
Match length  106
% identity    32
NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]
```

```
Seq. No.      399753
Seq. ID      LIB3431-027-P1-K1-F2
Method       BLASTX
NCBI GI      g3204108
BLAST score   570
E value      8.0e-59
Match length  118
% identity    87
NCBI Description (AJ006764) putative deoxycytidylate deaminase [Cicer
arietinum]
```

```
Seq. No.      399754
Seq. ID      LIB3431-027-P1-K1-F3
Method       BLASTX
NCBI GI      g132105
BLAST score   666
E value      5.0e-70
Match length  142
% identity    89
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                (D00643) small subunit of ribulose-1,5-bisphosphate
```

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 399755
 Seq. ID LIB3431-027-P1-K1-F4
 Method BLASTX
 NCBI GI g3789952
 BLAST score 307
 E value 6.0e-28
 Match length 66
 % identity 88
 NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No. 399756
 Seq. ID LIB3431-027-P1-K1-F5
 Method BLASTX
 NCBI GI g1076800
 BLAST score 717
 E value 5.0e-76
 Match length 155
 % identity 87
 NCBI Description L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -
 maize >gi_600116_emb_CAA84406_ (Z34934) cytosolic ascorbate
 peroxidase [Zea mays] >gi_1096503_prf_2111423A ascorbate
 peroxidase [Zea mays]

Seq. No. 399757
 Seq. ID LIB3431-027-P1-K1-F6
 Method BLASTX
 NCBI GI g1835731
 BLAST score 531
 E value 3.0e-54
 Match length 101
 % identity 100
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 399758
 Seq. ID LIB3431-027-P1-K1-F8
 Method BLASTX
 NCBI GI g3126854
 BLAST score 671
 E value 1.0e-70
 Match length 126
 % identity 100
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 399759
 Seq. ID LIB3431-027-P1-K1-F9
 Method BLASTX
 NCBI GI g6066383
 BLAST score 236
 E value 5.0e-20
 Match length 49
 % identity 98


```

NCBI GI          g5103831
BLAST score      281
E value          5.0e-25
Match length     94
% identity       60
NCBI Description (AC007591) ESTs gb_H37032, gb_R6425, gb_Z34651, gb_N37268,
gb_AA713172 and gb_Z34241 come from this gene. [Arabidopsis
thaliana]

```

Seq. No.	399766
Seq. ID	LIB3431-027-P1-K1-G6
Method	BLASTN
NCBI GI	g3075487
BLAST score	157
E value	5.0e-83
Match length	157
% identity	100
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

```
Seq. No.          399767
Seq. ID           LIB3431-027-P1-K1-G7
Method            BLASTX
NCBI GI           g5815133
BLAST score       183
E value           2.0e-13
Match length      99
% identity        37
NCBI Description   (AF169386) SPO11 [Mus musculus]
```

Seq. No.	399768
Seq. ID	LIB3431-027-P1-K1-G8
Method	BLASTX
NCBI GI	g3763918
BLAST score	236
E value	1.0e-19
Match length	67
% identity	70
NCBI Description	(AC004450) putative isopropylmalate dehydratase [Arabidopsis thaliana]

```
Seq. No.      399769
Seq. ID       LIB3431-027-P1-K1-H1
Method        BLASTX
NCBI GI       g1169544
BLAST score    540
E value       3.0e-55
Match length   154
% identity     67
NCBI Description ERD1 PROTEIN PRECURSOR >gi_541859_pir_JN0901 ERD1 protein
                - Arabidopsis thaliana >gi_497629_dbj_BAA04506_ (D17582)
                ERD1 protein [Arabidopsis thaliana]
```

```
Seq. No.      399770
Seq. ID      LIB3431-027-P1-K1-H11
Method       BLASTX
NCBI GI      q3075488
```

```
BLAST score      572
E value         1.0e-65
Match length    139
% identity      91
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
```

```
Seq. No.      399771
Seq. ID      LIB3431-027-P1-K1-H12
Method       BLASTX
NCBI GI      g3789954
BLAST score   148
E value      2.0e-19
Match length  118
% identity    53
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza
sativa]
```

```
Seq. No.      399772
Seq. ID      LIB3431-027-P1-K1-H3
Method       BLASTX
NCBI GI      g4587571
BLAST score   425
E value      8.0e-42
Match length  104
% identity    75
NCBI Description (AC006550) Belongs to the PF_01027 Uncharacterized protein
family UPF0005 with 7 transmembrane domains. [Arabidopsis
thaliana]
```

```
Seq. No.      399773
Seq. ID      LIB3431-027-P1-K1-H5
Method       BLASTX
NCBI GI      g115796
BLAST score   721
E value      2.0e-76
Match length  138
% identity    98
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I
                  CAB) (LHCP) >gi_218174_dbj_BAA00537_ (D00642) type II
                  light-harvesting chlorophyll a/b-binding protein [Oryza
                  sativa]
```

```
Seq. No.      399774
Seq. ID      LIB3431-027-P1-K1-H6
Method       BLASTX
NCBI GI      g3789954
BLAST score   186
E value      2.0e-14
Match length  64
% identity    61
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                sativa]
```

```
Seq. No.      399775
Seq. ID      LIB3431-027-P1-K1-H7
Method       BLASTX
NCBI GI      q3881189
```

```

BLAST score      489
E value          3.0e-49
Match length     144
% identity       61
NCBI Description (Z99281) similar to ADP-ribosylation factor; cDNA EST
                  EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337
                  comes from this gene; cDNA EST EMBL:C09829 comes from this
                  gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST y

```

```
Seq. No.      399776
Seq. ID      LIB3431-027-P1-K1-H8
Method       BLASTX
NCBI GI      g320618
BLAST score   489
E value      2.0e-49
Match length  109
% identity    85
NCBI Description  chlorophyll a/b-binding protein I precursor - rice
>gi_218172_dbj_BAA00536_(D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
>gi_227611_prf_1707316A chlorophyll a/b binding protein 1
[Oryza sativa]
```

```
Seq. No.      399777
Seq. ID      LIB3431-027-P1-K1-H9
Method       BLASTX
NCBI GI      g482311
BLAST score   731
E value      1.0e-77
Match length  142
% identity    100
NCBI Description  photosystem II oxygen-evolving complex protein 1 - rice
                  (strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
```

```
Seq. No.      399778
Seq. ID      LIB3431-027-P1-N1-A1
Method       BLASTX
NCBI GI      g687677
BLAST score   230
E value      4.0e-19
Match length  51
% identity    86
NCBI Description (U19925) unknown [Arabidopsis thaliana]
```

```
Seq. No.      399779
Seq. ID      LIB3431-027-P1-N1-A11
Method       BLASTX
NCBI GI      g3413423
BLAST score   169
E value      7.0e-12
Match length  64
% identity   48
NCBI Description (AJ006309) hypothetical protein [Arabidopsis thaliana]
```

Seq. No.	399780
Seq. ID	LIB3431-027-P1-N1-A12

Seq. No.	399785
Seq. ID	LIB3431-027-P1-N1-A8
Method	BLASTX
NCBI GI	g733454
BLAST score	271
E value	8.0e-24
Match length	56
% identity	95
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]
Seq. No.	399786
Seq. ID	LIB3431-027-P1-N1-A9
Method	BLASTX
NCBI GI	g3885892
BLAST score	338
E value	1.0e-31
Match length	65
% identity	100
NCBI Description	(AF093634) photosystem-1 F subunit precursor [Oryza sativa]
Seq. No.	399787
Seq. ID	LIB3431-027-P1-N1-B1
Method	BLASTX
NCBI GI	g482311
BLAST score	186
E value	6.0e-14
Match length	36
% identity	100
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]
Seq. No.	399788
Seq. ID	LIB3431-027-P1-N1-B10
Method	BLASTN
NCBI GI	g169798
BLAST score	42
E value	3.0e-14
Match length	94
% identity	86
NCBI Description	Oryza sativa 16.9 kDa heat shock protein gene, complete cds
Seq. No.	399789
Seq. ID	LIB3431-027-P1-N1-B2
Method	BLASTX
NCBI GI	g482311
BLAST score	154
E value	4.0e-10
Match length	44
% identity	73
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]
Seq. No.	399790
Seq. ID	LIB3431-027-P1-N1-B3


```
Seq. ID      LIB3431-027-P1-N1-D2
Method       BLASTX
NCBI GI      g1076724
BLAST score   284
E value      2.0e-25
Match length  56
% identity    95
NCBI Description LHCI-680, photosystem I antenna protein - barley
               >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
               antenna protein [Hordeum vulgare]
```

```
Seq. No.      399805
Seq. ID      LIB3431-027-P1-N1-D4
Method       BLASTX
NCBI GI      g548605
BLAST score   484
E value      1.0e-48
Match length  126
% identity    79
NCBI Description  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi_539055_pir_A48527 photosystem I protein psaK precursor
                  - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
```

```
Seq. No.      399806
Seq. ID      LIB3431-027-P1-N1-D7
Method       BLASTX
NCBI GI      g3036951
BLAST score   343
E value      2.0e-32
Match length  65
% identity    100
NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein
[Nicotiana glauca]
```

```
Seq. No.          399807
Seq. ID           LIB3431-027-P1-N1-D8
Method            BLASTX
NCBI GI           g421916
BLAST score       243
E value           1.0e-20
Match length      45
% identity        100
NCBI Description   chlorophyll a/b-binding protein - English ivy (fragment)
                  >gi_12582_emb_CAA48410_ (X68333) light harvesting
                  chlorophyll a/b binding protein [Hedera helix]
```

```
Seq. No.      399808
Seq. ID      LIB3431-027-P1-N1-E1
Method       BLASTN
NCBI GI      g2570510
BLAST score   150
E value      8.0e-79
Match length  226
% identity    92
NCBI Description  Oryza sativa chlorophyll a-b binding protein mRNA, complete
```

09084016 101000

```
Seq. No.      399810
Seq. ID      LIB3431-027-P1-N1-E12
Method       BLASTX
NCBI GI      g132105
BLAST score   169
E value      2.0e-20
Match length 55
% identity   98
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]
```

```
Seq. No.          399811
Seq. ID           LIB3431-027-P1-N1-E4
Method            BLASTN
NCBI GI           g2570514
BLAST score       266
E value           1.0e-148
Match length      369
% identity         98
NCBI Description   Oryza sativa glycolate oxidase (GOX) mRNA, complete cds
```

```
Seq. No.          399812
Seq. ID           LIB3431-027-P1-N1-E5
Method            BLASTX
NCBI GI           g451193
BLAST score       284
E value           2.0e-25
Match length      87
% identity        66
NCBI Description   (L28008) wali7 [Triticum aestivum]
                  >gi 1090845 prf 2019486B wali7 gene [Triticum aestivum]
```

```
Seq. No.      399813
Seq. ID      LIB3431-027-P1-N1-E6
Method       BLASTX
NCBI GI      g5354158
BLAST score   155
E value      3.0e-10
```


00000000000000000000000000000000

```
Seq. No.      399820
Seq. ID      LIB3431-027-P1-N1-F3
Method       BLASTN
NCBI GI      g218207
BLAST score   195
E value      1.0e-105
Match length  315
% identity    90
NCBI Description  Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS1139
```

```
Seq. No.          399821
Seq. ID           LIB3431-027-P1-N1-F4
Method            BLASTN
NCBI GI           g3789951
BLAST score       134
E value           4.0e-69
Match length      318
% identity        86
NCBI Description   Oryza sativa chlorophyll a/b-binding protein presursor
                  (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
```

```
Seq. No.      399822
Seq. ID       LIB3431-027-P1-N1-F5
Method        BLASTN
NCBI GI       g433216
BLAST score   223
E value       1.0e-122
Match length  232
% identity    99
NCBI Description  Rice mRNA for ascorbate peroxidase (gene name SS622),
                  partial cds
```

```
Seq. No.      399823
Seq. ID      LIB3431-027-P1-N1-F6
Method       BLASTX
NCBI GI      g1835731
BLAST score   326
E value      3.0e-30
Match length  73
% identity    86
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
```

Seq. No. 399824
 Seq. ID LIB3431-027-P1-N1-F8
 Method BLASTX
 NCBI GI g3126854
 BLAST score 333
 E value 5.0e-31
 Match length 63
 % identity 100
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 399825
 Seq. ID LIB3431-027-P1-N1-F9
 Method BLASTX
 NCBI GI g6066383
 BLAST score 236
 E value 5.0e-20
 Match length 49
 % identity 98
 NCBI Description (AJ011926) Mg-protoporphyrin IX [Hordeum vulgare]

Seq. No. 399826
 Seq. ID LIB3431-027-P1-N1-G1
 Method BLASTN
 NCBI GI g2624327
 BLAST score 319
 E value 1.0e-179
 Match length 322
 % identity 100
 NCBI Description Oryza sativa mRNA for glycine rich RNA-binding protein 2 (OsGRP2)

Seq. No. 399827
 Seq. ID LIB3431-027-P1-N1-G11
 Method BLASTN
 NCBI GI g3789951
 BLAST score 193
 E value 1.0e-104
 Match length 391
 % identity 95
 NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 399828
 Seq. ID LIB3431-027-P1-N1-G12
 Method BLASTX
 NCBI GI g3789954
 BLAST score 339
 E value 9.0e-32
 Match length 63
 % identity 100
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 399829
 Seq. ID LIB3431-027-P1-N1-G4

00001016-101000

Method BLASTX
NCBI GI g2832672
BLAST score 183
E value 2.0e-13
Match length 37
% identity 97
NCBI Description (AL021712) nifU-like protein [Arabidopsis thaliana]

Seq. No. 399830
Seq. ID LIB3431-027-P1-N1-G6
Method BLASTN
NCBI GI g3075487
BLAST score 149
E value 3.0e-78
Match length 157
% identity 99
NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69)
mRNA, complete cds

Seq. No. 399831
Seq. ID LIB3431-027-P1-N1-G8
Method BLASTX
NCBI GI g3763918
BLAST score 225
E value 3.0e-18
Match length 70
% identity 64
NCBI Description (AC004450) putative isopropylmalate dehydratase
[Arabidopsis thaliana]

Seq. No. 399832
Seq. ID LIB3431-027-P1-N1-H1
Method BLASTX
NCBI GI g733454
BLAST score 383
E value 6.0e-37
Match length 80
% identity 93
NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
[Zea mays]

Seq. No. 399833
Seq. ID LIB3431-027-P1-N1-H11
Method BLASTN
NCBI GI g3075487
BLAST score 310
E value 1.0e-174
Match length 314
% identity 100
NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69)
mRNA, complete cds

Seq. No. 399834
Seq. ID LIB3431-027-P1-N1-H12
Method BLASTX
NCBI GI g517500
BLAST score 347

09534-01

```
Seq. No.          399851
Seq. ID           LIB3431-028-P1-K1-B5
Method            BLASTX
NCBI GI           g2499775
BLAST score       188
E value           5.0e-14
Match length      84
% identity        49
NCBI Description  51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL
                  CIS-TRANS ISOMERASE) (PPIASE) (ROTAMASE) >gi_915280
                  (U16959) FKBP51 [Mus musculus] >gi_1020307 (U36220) FK506
                  binding protein 51 [Mus musculus]
```

```
Seq. No.      399852
Seq. ID      LIB3431-028-P1-K1-C1
Method       BLASTX
NCBI GI      g5802955
BLAST score   194
E value      8.0e-15
Match length  79
% identity    47
NCBI Description (AF178990) stress related protein [Vitis riparia]
```

Seq. No.	399853
Seq. ID	LIB3431-028-P1-K1-C10
Method	BLASTX
NCBI GI	g2734085
BLAST score	154
E value	5.0e-10
Match length	107
% identity	28
NCBI Description	(AF003136) contains similarity to ATP synthase subunit B [Caenorhabditis elegans]

```
Seq. No.      399854
Seq. ID      LIB3431-028-P1-K1-C12
Method       BLASTN
NCBI GI      g6015437
BLAST score   35
E value      6.0e-10
Match length  35
% identity   100
NCBI Description Homo sapiens PEX1 mRNA, complete cds
```

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[Hordeum vulgare]

Seq. No. 399865
 Seq. ID LIB3431-028-P1-K1-D5
 Method BLASTN
 NCBI GI g3885891
 BLAST score 119
 E value 2.0e-60
 Match length 156
 % identity 100
 NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds

Seq. No. 399866
 Seq. ID LIB3431-028-P1-K1-D6
 Method BLASTX
 NCBI GI g2501189
 BLAST score 164
 E value 7.0e-12
 Match length 33
 % identity 91
 NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
 >gi_2130146_pir_S61419 thiamine biosynthetic enzyme thil-1
 - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
 [Zea mays]

Seq. No. 399867
 Seq. ID LIB3431-028-P1-K1-D7
 Method BLASTX
 NCBI GI g3341692
 BLAST score 324
 E value 6.0e-30
 Match length 141
 % identity 54
 NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]

Seq. No. 399868
 Seq. ID LIB3431-028-P1-K1-D8
 Method BLASTX
 NCBI GI g2570511
 BLAST score 660
 E value 9.0e-72
 Match length 138
 % identity 97
 NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No. 399869
 Seq. ID LIB3431-028-P1-K1-D9
 Method BLASTX
 NCBI GI g1076800
 BLAST score 561
 E value 1.0e-57
 Match length 121
 % identity 85
 NCBI Description L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -
 maize >gi_600116_emb_CAA84406_ (Z34934) cytosolic ascorbate
 peroxidase [Zea mays] >gi_1096503_prf_2111423A ascorbate


```
% identity      59
NCBI Description (AC002561) similar to Drosophila couch potato protein
                  [Arabidopsis thaliana]
```

```
Seq. No.      399885
Seq. ID      LIB3431-028-P1-K1-F8
Method       BLASTX
NCBI GI      g3033382
BLAST score   257
E value      4.0e-22
Match length  101
% identity    49
NCBI Description (AC004238) unknown protein [Arabidopsis thaliana]
```

```
Seq. No.      399886
Seq. ID      LIB3431-028-P1-K1-G1
Method       BLASTX
NCBI GI      g6006894
BLAST score   404
E value      2.0e-39
Match length  113
% identity    75
NCBI Description (AC008153) unknown protein [Arabidopsis thaliana]
```

Seq. No.	399887
Seq. ID	LIB3431-028-P1-K1-G10
Method	BLASTX
NCBI GI	g168523
BLAST score	274
E value	3.0e-24
Match length	113
% identity	55
NCBI Description	(M31483) glyceraldehyde-3-phosphate dehydrogenase precursor [Zea mays]

```
Seq. No.      399888
Seq. ID      LIB3431-028-P1-K1-G12
Method       BLASTX
NCBI GI      g2072555
BLAST score   237
E value      7.0e-20
Match length  44
% identity    100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
protein [Oryza sativa]
```

```
Seq. No.      399889
Seq. ID       LIB3431-028-P1-K1-G2
Method        BLASTX
NCBI GI       g2293480
BLAST score   413
E value       1.0e-40
Match length  86
% identity    93
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
```


E value 1.0e-12
 Match length 104
 % identity 48
 NCBI Description (AC006587) putative protein kinase [Arabidopsis thaliana]

Seq. No. 399896
 Seq. ID LIB3431-028-P1-K1-H1
 Method BLASTX
 NCBI GI g586038
 BLAST score 537
 E value 6.0e-55
 Match length 148
 % identity 72
 NCBI Description SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN, CHLOROPLAST PRECURSOR (SRP54) (54 CHLOROPLAST PROTEIN) (54CP) (FFC) >gi_480296_pir_S36637 signal recognition particle 54CP protein precursor - Arabidopsis thaliana >gi_396701_emb_CAA79981.1_ (Z21970) 54CP [Arabidopsis thaliana]

Seq. No. 399897
 Seq. ID LIB3431-028-P1-K1-H10
 Method BLASTX
 NCBI GI g132105
 BLAST score 609
 E value 2.0e-63
 Match length 131
 % identity 88
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 399898
 Seq. ID LIB3431-028-P1-K1-H11
 Method BLASTX
 NCBI GI g1170606
 BLAST score 314
 E value 8.0e-29
 Match length 81
 % identity 77
 NCBI Description ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE) >gi_629863_pir_S45634 adenylate kinase (EC 2.7.4.3), chloroplast - maize >gi_3114421_pdb_1ZAK A Chain A, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a) >gi_3114422_pdb_1ZAK B Chain B, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a)

Seq. No. 399899
 Seq. ID LIB3431-028-P1-K1-H12

Match length 418
 % identity 100
 NCBI Description Genomic Sequence For Oryza sativa Clone 10P20, Lemont Strain, Complete Sequence, complete sequence

Seq. No. 399910
 Seq. ID LIB3431-028-P1-N1-A11
 Method BLASTX
 NCBI GI g2462750
 BLAST score 173
 E value 2.0e-12
 Match length 51
 % identity 67
 NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 399911
 Seq. ID LIB3431-028-P1-N1-A12
 Method BLASTX
 NCBI GI g3643602
 BLAST score 246
 E value 7.0e-21
 Match length 78
 % identity 58
 NCBI Description (AC005395) putative tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No. 399912
 Seq. ID LIB3431-028-P1-N1-A4
 Method BLASTX
 NCBI GI g3808101
 BLAST score 344
 E value 2.0e-32
 Match length 79
 % identity 90
 NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]

Seq. No. 399913
 Seq. ID LIB3431-028-P1-N1-A6
 Method BLASTX
 NCBI GI g1835731
 BLAST score 286
 E value 1.0e-25
 Match length 65
 % identity 85
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 399914
 Seq. ID LIB3431-028-P1-N1-B1
 Method BLASTX
 NCBI GI g3345477
 BLAST score 277
 E value 1.0e-24
 Match length 52
 % identity 100
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

0966016 30000

```
Seq. No.      399921
Seq. ID       LIB3431-028-P1-N1-C4
Method        BLASTX
NCBI GI       g693920
BLAST score    327
E value       2.0e-30
Match length  64
% identity    98
NCBI Description (U21113) chlorophyll a/b binding protein [Solanum
tuberosum]
```

Seq. No.	399922
Seq. ID	LIB3431-028-P1-N1-C5
Method	BLASTX
NCBI GI	g1835731
BLAST score	330
E value	1.0e-30
Match length	74
% identity	86
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

```
Seq. No.          399923
Seq. ID           LIB3431-028-P1-N1-C7
Method            BLASTX
NCBI GI           g132166
BLAST score       160
E value           6.0e-11
Match length      31
% identity        87
NCBI Description  RIBULOSE BISPHTHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
                  >gi_81660_pir_S04048 ribulose-bisphosphate carboxylase
                  activase precursor - Arabidopsis thaliana
                  >gi_16471_emb_CAA32429_(X14212) rubisco activase (AA 1 -
                  473) [Arabidopsis thaliana]
```

51175

Method BLASTX
 NCBI GI g3885892
 BLAST score 261
 E value 1.0e-22
 Match length 53
 % identity 98
 NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 399930
 Seq. ID LIB3431-028-P1-N1-D6
 Method BLASTX
 NCBI GI g2501190
 BLAST score 198
 E value 3.0e-15
 Match length 57
 % identity 74
 NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
 >gi_2130147_pir_S61420 thiamine biosynthetic enzyme thil-2
 - maize >gi_596080 (U17351) thiamine biosynthetic enzyme
 [Zea mays]

Seq. No. 399931
 Seq. ID LIB3431-028-P1-N1-D8
 Method BLASTX
 NCBI GI g115793
 BLAST score 396
 E value 2.0e-38
 Match length 78
 % identity 95
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR
 (CAB) >gi_72749_pir_CDBH3 chlorophyll a/b-binding protein
 type III precursor - barley >gi_19023_emb_CAA44881
 (X63197) type III LHCII CAB precursor protein [Hordeum
 vulgare]

Seq. No. 399932
 Seq. ID LIB3431-028-P1-N1-D9
 Method BLASTN
 NCBI GI g433216
 BLAST score 165
 E value 9.0e-88
 Match length 171
 % identity 99
 NCBI Description Rice mRNA for ascorbate peroxidase (gene name SS622),
 partial cds

Seq. No. 399933
 Seq. ID LIB3431-028-P1-N1-E1
 Method BLASTX
 NCBI GI g132105
 BLAST score 301
 E value 2.0e-27
 Match length 57
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 399934
Seq. ID LIB3431-028-P1-N1-E3
Method BLASTX
NCBI GI g2499417
BLAST score 323
E value 5.0e-30
Match length 74
% identity 82
NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
>gi_1085826_pir_S49248 H-protein - Flaveria anomala
>gi_547558_emb_CAA85761_ (Z37524) H-protein [Flaveria
anomala]

Seq. No. 399935
Seq. ID LIB3431-028-P1-N1-E4
Method BLASTX
NCBI GI g289920
BLAST score 315
E value 5.0e-29
Match length 64
% identity 95
NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium
hirsutum]

Seq. No. 399936
Seq. ID LIB3431-028-P1-N1-E5
Method BLASTX
NCBI GI g2129703
BLAST score 189
E value 3.0e-14
Match length 87
% identity 49
NCBI Description receptor kinase - Arabidopsis thaliana
>gi_2129704_pir_S71184 receptor kinase - Arabidopsis
thaliana >gi_166692 (M80238) receptor kinase [Arabidopsis
thaliana] >gi_445123_prf_1908429A receptor kinase
[Arabidopsis thaliana]

Seq. No. 399937
Seq. ID LIB3431-028-P1-N1-E6
Method BLASTX
NCBI GI g3789954
BLAST score 357
E value 7.0e-34
Match length 66
% identity 100
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza
sativa]

Seq. No. 399938

Method BLASTX
NCBI GI g5442410
BLAST score 182
E value 2.0e-13
Match length 78
% identity 50
NCBI Description (AF159254) ascorbate peroxidase [Zantedeschia aethiopica]

Seq. No. 399943
Seq. ID LIB3431-028-P1-N1-F5
Method BLASTX
NCBI GI g548603
BLAST score 158
E value 1.0e-10
Match length 34
% identity 91
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
(PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
>gi_478404_pir_JQ2247 photosystem I chain D precursor -
barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 399944
Seq. ID LIB3431-028-P1-N1-F8
Method BLASTX
NCBI GI g3033382
BLAST score 359
E value 3.0e-34
Match length 76
% identity 86
NCBI Description (AC004238) unknown protein [Arabidopsis thaliana]

Seq. No. 399945
Seq. ID LIB3431-028-P1-N1-F9
Method BLASTX
NCBI GI g1076724
BLAST score 374
E value 7.0e-36
Match length 72
% identity 94
NCBI Description LHCI-680, photosystem I antenna protein - barley
>gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
antenna protein [Hordeum vulgare]

Seq. No. 399946
Seq. ID LIB3431-028-P1-N1-G10
Method BLASTX
NCBI GI g120661
BLAST score 180
E value 4.0e-13
Match length 38
% identity 87
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST
PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate
dehydrogenase A-subunit precursor [Nicotiana tabacum]

Seq. No. 399947
Seq. ID LIB3431-028-P1-N1-G12

Seq. No. 399958
 Seq. ID LIB3431-028-P1-N1-H3
 Method BLASTX
 NCBI GI g4079798
 BLAST score 183
 E value 1.0e-13
 Match length 34
 % identity 100
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 399959
 Seq. ID LIB3431-028-P1-N1-H4
 Method BLASTX
 NCBI GI g1351270
 BLAST score 149
 E value 1.0e-09
 Match length 30
 % identity 100
 NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
 >gi_478410_pir_JQ2255 triose-phosphate isomerase (EC 5.3.1.1) - rice >gi_169821 (M87064) triosephosphate isomerase [Oryza sativa]

Seq. No. 399960
 Seq. ID LIB3431-028-P1-N1-H5
 Method BLASTX
 NCBI GI g871931
 BLAST score 199
 E value 2.0e-15
 Match length 65
 % identity 66
 NCBI Description (D30763) ferredoxin [Oryza sativa]

Seq. No. 399961
 Seq. ID LIB3431-028-P1-N1-H6
 Method BLASTX
 NCBI GI g417260
 BLAST score 247
 E value 5.0e-21
 Match length 65
 % identity 71
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

Seq. No. 399962
 Seq. ID LIB3431-028-P1-N1-H9
 Method BLASTX
 NCBI GI g4079798
 BLAST score 268
 E value 2.0e-23
 Match length 52
 % identity 98
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

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Seq. No.          399963
Seq. ID           LIB3431-029-P1-K1-A1
Method            BLASTN
NCBI GI           g2570516
BLAST score       55
E value           2.0e-22
Match length      125
% identity        87
NCBI Description   Oryza sativa thioredoxin F isoform mRNA, complete cds

Seq. No.          399964
Seq. ID           LIB3431-029-P1-K1-A10
Method            BLASTX
NCBI GI           g2982362
BLAST score       444
E value           4.0e-44
Match length      91
% identity        89
NCBI Description   (AF053311) glutathione peroxidase [Zantedeschia aethiopica]

Seq. No.          399965
Seq. ID           LIB3431-029-P1-K1-A11
Method            BLASTN
NCBI GI           g473980
BLAST score       74
E value           1.0e-33
Match length      115
% identity        90
NCBI Description   Rice mRNA, partial homologous to glycine-rich protein gene

Seq. No.          399966
Seq. ID           LIB3431-029-P1-K1-A5
Method            BLASTX
NCBI GI           g2501189
BLAST score       383
E value           6.0e-37
Match length      111
% identity        69
NCBI Description   THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
>gi_2130146_pir_S61419 thiamine biosynthetic enzyme thil-1
- maize >gi_596078 (U17350) thiamine biosynthetic enzyme
[Zea mays]

Seq. No.          399967
Seq. ID           LIB3431-029-P1-K1-A8
Method            BLASTX
NCBI GI           g3075488
BLAST score       270
E value           2.0e-47
Match length      117
% identity        82
NCBI Description   (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No.          399968
Seq. ID           LIB3431-029-P1-K1-B1
Method            BLASTX

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NCBI GI g3292814
 BLAST score 540
 E value 3.0e-55
 Match length 144
 % identity 72
 NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 399969
 Seq. ID LIB3431-029-P1-K1-B11
 Method BLASTX
 NCBI GI g2662343
 BLAST score 639
 E value 7.0e-67
 Match length 124
 % identity 100
 NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 399970
 Seq. ID LIB3431-029-P1-K1-B12
 Method BLASTX
 NCBI GI g5734634
 BLAST score 286
 E value 2.0e-25
 Match length 83
 % identity 60
 NCBI Description (AP000391) Similar to putative lipase (AC006232) [Oryza sativa]

Seq. No. 399971
 Seq. ID LIB3431-029-P1-K1-B3
 Method BLASTX
 NCBI GI g1084455
 BLAST score 527
 E value 9.0e-54
 Match length 115
 % identity 88
 NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
 >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]

Seq. No. 399972
 Seq. ID LIB3431-029-P1-K1-B4
 Method BLASTX
 NCBI GI g132105
 BLAST score 566
 E value 2.0e-58
 Match length 131
 % identity 82
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Match length 142
 % identity 97
 NCBI Description photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No. 399983
 Seq. ID LIB3431-029-P1-K1-D8
 Method BLASTX
 NCBI GI g132105
 BLAST score 565
 E value 3.0e-58
 Match length 124
 % identity 85
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 399984
 Seq. ID LIB3431-029-P1-K1-E10
 Method BLASTX
 NCBI GI g132105
 BLAST score 609
 E value 2.0e-63
 Match length 131
 % identity 88
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 399985
 Seq. ID LIB3431-029-P1-K1-E11
 Method BLASTX
 NCBI GI g1617206
 BLAST score 190
 E value 6.0e-23
 Match length 74
 % identity 76
 NCBI Description (Z72489) CP12 [Pisum sativum]

Seq. No. 399986
 Seq. ID LIB3431-029-P1-K1-E12
 Method BLASTX
 NCBI GI g2407281
 BLAST score 497

NCBI Description (AC006841) putative serine/threonine protein kinase
[Arabidopsis thaliana]

Seq. No. 399992
Seq. ID LIB3431-029-P1-K1-F12
Method BLASTX
NCBI GI g3063447
BLAST score 244
E value 2.0e-33
Match length 155
% identity 24
NCBI Description (AC003981) F22013.9 [Arabidopsis thaliana]

Seq. No. 399993
Seq. ID LIB3431-029-P1-K1-F2
Method BLASTX
NCBI GI g1617197
BLAST score 304
E value 1.0e-27
Match length 76
% identity 76
NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 399994
Seq. ID LIB3431-029-P1-K1-F3
Method BLASTN
NCBI GI g2407266
BLAST score 102
E value 3.0e-50
Match length 158
% identity 91
NCBI Description Oryza sativa low molecular early light-inducible protein
mRNA, complete cds

Seq. No. 399995
Seq. ID LIB3431-029-P1-K1-F4
Method BLASTX
NCBI GI g729478
BLAST score 230
E value 5.0e-19
Match length 120
% identity 42
NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
>gi_442481_dbj_BAA04616 (D17790) ferredoxin-NADP+
reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_
(AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to
a region of the predicted gene.; similar to
ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

Seq. No. 399996
Seq. ID LIB3431-029-P1-K1-F5
Method BLASTX
NCBI GI g3789954
BLAST score 654
E value 1.0e-68
Match length 121
% identity 100

00684015.101000

NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 399997
Seq. ID LIB3431-029-P1-K1-F6
Method BLASTX
NCBI GI g2570511
BLAST score 514
E value 2.0e-52
Match length 98
% identity 99

NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No. 399998
Seq. ID LIB3431-029-P1-K1-F8
Method BLASTX
NCBI GI g131176
BLAST score 322
E value 9.0e-30
Match length 62
% identity 98

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
>gi_72683_pir_F1BH4 photosystem I chain IV precursor - barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf_1413233A 10.8kD photosystem I protein [Hordeum vulgare var. distichum]

Seq. No. 399999
Seq. ID LIB3431-029-P1-K1-F9
Method BLASTX
NCBI GI g3850621
BLAST score 450
E value 9.0e-45
Match length 127
% identity 69

NCBI Description (Y15382) putative RNA binding protein [Arabidopsis thaliana]

Seq. No. 400000
Seq. ID LIB3431-029-P1-K1-G10
Method BLASTX
NCBI GI g3075488
BLAST score 713
E value 1.0e-75
Match length 143
% identity 97

NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 400001
Seq. ID LIB3431-029-P1-K1-G11
Method BLASTX
NCBI GI g4406764
BLAST score 293
E value 3.0e-26
Match length 80

Seq. No. 400012
 Seq. ID LIB3431-029-P1-K1-H3
 Method BLASTX
 NCBI GI g132105
 BLAST score 546
 E value 6.0e-56
 Match length 122
 % identity 84
 NCBI Description RIBULOSE BISPHTOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 400013
 Seq. ID LIB3431-029-P1-K1-H5
 Method BLASTN
 NCBI GI g168500
 BLAST score 62
 E value 3.0e-26
 Match length 118
 % identity 88
 NCBI Description Maize (Zea mays) histone H4 gene (H4C14), complete cds

Seq. No. 400014
 Seq. ID LIB3431-029-P1-K1-H7
 Method BLASTX
 NCBI GI g5926740
 BLAST score 455
 E value 2.0e-45
 Match length 89
 % identity 98
 NCBI Description (AB025310) asparaginyl endopeptidase [Oryza sativa]

Seq. No. 400015
 Seq. ID LIB3431-029-P1-N1-A10
 Method BLASTX
 NCBI GI g2982362
 BLAST score 306
 E value 6.0e-28
 Match length 63
 % identity 89
 NCBI Description (AF053311) glutathione peroxidase [Zantedeschia aethiopica]

Seq. No. 400016
 Seq. ID LIB3431-029-P1-N1-A2
 Method BLASTX
 NCBI GI g4469021
 BLAST score 271
 E value 6.0e-24
 Match length 75
 % identity 71

NCBI GI g3850621
 BLAST score 177
 E value 7.0e-13
 Match length 39
 % identity 87
 NCBI Description (Y15382) putative RNA binding protein [Arabidopsis thaliana]

Seq. No. 400052
 Seq. ID LIB3431-029-P1-N1-G1
 Method BLASTX
 NCBI GI g115813
 BLAST score 233
 E value 2.0e-19
 Match length 53
 % identity 85
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_(X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 400053
 Seq. ID LIB3431-029-P1-N1-G10
 Method BLASTN
 NCBI GI g3075487
 BLAST score 75
 E value 5.0e-34
 Match length 94
 % identity 97
 NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No. 400054
 Seq. ID LIB3431-029-P1-N1-G12
 Method BLASTN
 NCBI GI g20262
 BLAST score 173
 E value 2.0e-92
 Match length 345
 % identity 88
 NCBI Description O.sativa light-induced mRNA

Seq. No. 400055
 Seq. ID LIB3431-029-P1-N1-G2
 Method BLASTX
 NCBI GI g3036946
 BLAST score 314
 E value 6.0e-29
 Match length 61
 % identity 98
 NCBI Description (AB012637) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 400056
 Seq. ID LIB3431-029-P1-N1-G3
 Method BLASTN
 NCBI GI g2072554
 BLAST score 142

Match length 66
 % identity 68
 NCBI Description (D30763) ferredoxin [Oryza sativa]

Seq. No. 400073
 Seq. ID LIB3431-030-P1-K2-A9
 Method BLASTX
 NCBI GI g671740
 BLAST score 638
 E value 9.0e-67
 Match length 119
 % identity 99
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 400074
 Seq. ID LIB3431-030-P1-K2-B1
 Method BLASTN
 NCBI GI g2407280
 BLAST score 43
 E value 2.0e-15
 Match length 90
 % identity 88
 NCBI Description Oryza sativa ribulose 1,5-bisphosphate carboxylase small subunit mRNA, complete cds

Seq. No. 400075
 Seq. ID LIB3431-030-P1-K2-B2
 Method BLASTX
 NCBI GI g2832681
 BLAST score 414
 E value 2.0e-40
 Match length 89
 % identity 82
 NCBI Description (AL021712) putative protein [Arabidopsis thaliana]

Seq. No. 400076
 Seq. ID LIB3431-030-P1-K2-B3
 Method BLASTN
 NCBI GI g6103440
 BLAST score 87
 E value 1.0e-41
 Match length 95
 % identity 98
 NCBI Description Oryza sativa metallothionein-like protein (ML2) mRNA, complete cds

Seq. No. 400077
 Seq. ID LIB3431-030-P1-K2-B4
 Method BLASTN
 NCBI GI g5734616
 BLAST score 227
 E value 1.0e-125
 Match length 235
 % identity 99
 NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01

Seq. No. 400078
 Seq. ID LIB3431-030-P1-K2-B8
 Method BLASTX
 NCBI GI g132105
 BLAST score 547
 E value 4.0e-56
 Match length 120
 % identity 86
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 400079
 Seq. ID LIB3431-030-P1-K2-C10
 Method BLASTX
 NCBI GI g4678303
 BLAST score 184
 E value 1.0e-13
 Match length 52
 % identity 63
 NCBI Description (AL049655) putative protein [Arabidopsis thaliana]

Seq. No. 400080
 Seq. ID LIB3431-030-P1-K2-C11
 Method BLASTN
 NCBI GI g19086
 BLAST score 78
 E value 1.0e-35
 Match length 126
 % identity 91
 NCBI Description Hordeum vulgare pot. psaE mRNA

Seq. No. 400081
 Seq. ID LIB3431-030-P1-K2-C2
 Method BLASTN
 NCBI GI g19094
 BLAST score 54
 E value 1.0e-21
 Match length 66
 % identity 95
 NCBI Description H.vulgare mRNA PsaN for photosystem I subunit N

Seq. No. 400082
 Seq. ID LIB3431-030-P1-K2-C4
 Method BLASTX
 NCBI GI g4678303
 BLAST score 205
 E value 4.0e-16
 Match length 57
 % identity 65
 NCBI Description (AL049655) putative protein [Arabidopsis thaliana]

09634016 101000

Seq. No. 400083
 Seq. ID LIB3431-030-P1-K2-C6
 Method BLASTX
 NCBI GI g2501189
 BLAST score 618
 E value 2.0e-64
 Match length 129
 % identity 92
 NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
 >gi_2130146_pir_S61419 thiamine biosynthetic enzyme thil-1
 - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
 [Zea mays]

Seq. No. 400084
 Seq. ID LIB3431-030-P1-K2-C7
 Method BLASTX
 NCBI GI g4960154
 BLAST score 316
 E value 3.0e-29
 Match length 97
 % identity 65
 NCBI Description (AF153283) putative progesterone-binding protein homolog
 [Arabidopsis thaliana]

Seq. No. 400085
 Seq. ID LIB3431-030-P1-K2-C8
 Method BLASTX
 NCBI GI g3776581
 BLAST score 335
 E value 3.0e-31
 Match length 100
 % identity 61
 NCBI Description (AC005388) Similar to Beta integral membrane protein
 homolog gb_U43629 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 400086
 Seq. ID LIB3431-030-P1-K2-C9
 Method BLASTN
 NCBI GI g6016845
 BLAST score 271
 E value 1.0e-151
 Match length 285
 % identity 99
 NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No. 400087
 Seq. ID LIB3431-030-P1-K2-D10
 Method BLASTX
 NCBI GI g3126854
 BLAST score 650
 E value 3.0e-68
 Match length 124
 % identity 98
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 400088

>gi_1375075_dbj_BAA12870.1_ (D85763) glyoxysomal malate dehydrogenase [Oryza sativa]

Seq. No. 400102
 Seq. ID LIB3431-030-P1-K2-F1
 Method BLASTX
 NCBI GI g133999
 BLAST score 489
 E value 2.0e-49
 Match length 99
 % identity 100
 NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S7 >gi_70904_pir_R3RZ7 ribosomal protein S7 - rice chloroplast
 >gi_12037_emb_CAA33942_ (X15901) ribosomal protein S7 [Oryza sativa] >gi_12065_emb_CAA33919_ (X15901) ribosomal protein S7 [Oryza sativa] >gi_226657_prf_1603356CH ribosomal protein S7 [Oryza sativa]

Seq. No. 400103
 Seq. ID LIB3431-030-P1-K2-F10
 Method BLASTX
 NCBI GI g132105
 BLAST score 706
 E value 1.0e-74
 Match length 131
 % identity 98
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 400104
 Seq. ID LIB3431-030-P1-K2-F12
 Method BLASTX
 NCBI GI g1519251
 BLAST score 443
 E value 6.0e-44
 Match length 111
 % identity 83
 NCBI Description (U65957) GF14-c protein [Oryza sativa]

Seq. No. 400105
 Seq. ID LIB3431-030-P1-K2-F2
 Method BLASTN
 NCBI GI g3789951
 BLAST score 71
 E value 3.0e-32
 Match length 91
 % identity 95
 NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

09684016.101000

Seq. No. 400106
Seq. ID LIB3431-030-P1-K2-F4
Method BLASTX
NCBI GI g2570523
BLAST score 567
E value 2.0e-58
Match length 128
% identity 80
NCBI Description (AF022873) inorganic phosphate transporter [Lycopersicon
esculentum]

Seq. No. 400107
Seq. ID LIB3431-030-P1-K2-F5
Method BLASTX
NCBI GI g134944
BLAST score 718
E value 6.0e-82
Match length 179
% identity 84
NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
(STEAROYL-ACP DESATURASE) >gi_100502_pir_A39173
acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6)
precursor - safflower >gi_167197 (M61109)
stearyl-acyl-carrier protein desaturase [Carthamus
tinctorius]

Seq. No. 400108
Seq. ID LIB3431-030-P1-K2-F6
Method BLASTX
NCBI GI g3777598
BLAST score 314
E value 6.0e-29
Match length 104
% identity 67
NCBI Description (AF095707) 30S ribosomal protein S17 [Oryza sativa]

Seq. No. 400109
Seq. ID LIB3431-030-P1-K2-F7
Method BLASTX
NCBI GI g3789952
BLAST score 279
E value 1.0e-45
Match length 102
% identity 96
NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza
sativa]

Seq. No. 400110
Seq. ID LIB3431-030-P1-K2-F8
Method BLASTX
NCBI GI g3024697
BLAST score 274
E value 2.0e-24
Match length 91
% identity 65
NCBI Description T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON)

E value	1.0e-154
Match length	345
% identity	96
NCBI Description	Oryza sativa triosephosphate isomerase (Rictpi) mRNA, complete cds

```
Seq. No.      400126
Seq. ID      LIB3431-030-P1-N1-A2
Method       BLASTX
NCBI GI      g115787
BLAST score   403
E value      3.0e-39
Match length  76
% identity    100
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
```

```
Seq. No.      400127
Seq. ID      LIB3431-030-P1-N1-A4
Method       BLASTX
NCBI GI      g3126854
BLAST score   339
E value      1.0e-31
Match length  64
% identity    100
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```

Seq. No.	400128
Seq. ID	LIB3431-030-P1-N1-A5
Method	BLASTN
NCBI GI	g5922603
BLAST score	57
E value	4.0e-23
Match length	80
% identity	94
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0705D01

```
Seq. No.      400129
Seq. ID      LIB3431-030-P1-N1-A6
Method       BLASTX
NCBI GI      g729478
BLAST score   323
E value      6.0e-30
Match length  73
% identity    79
NCBI Description  FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
>gi_442481 dbj_BAA04616_ (D17790) ferredoxin-NADP+
reductase [Oryza sativa] >gi_6069649 dbj_BAA85425.1_
(AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to
a region of the predicted gene.; similar to
ferredoxin-NADP+ reductase (D17790) [Oryza sativa]
```

Seq. No. 400130
Seq. ID LIB3431-030-P1-N1-A7

protein [Oryza sativa]

Seq. No. 400135
 Seq. ID LIB3431-030-P1-N1-B4
 Method BLASTN
 NCBI GI g5734616
 BLAST score 409
 E value 0.0e+00
 Match length 499
 % identity 100
 NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01

Seq. No. 400136
 Seq. ID LIB3431-030-P1-N1-B5
 Method BLASTX
 NCBI GI g3345477
 BLAST score 331
 E value 9.0e-31
 Match length 62
 % identity 100
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 400137
 Seq. ID LIB3431-030-P1-N1-B7
 Method BLASTX
 NCBI GI g3510256
 BLAST score 229
 E value 9.0e-19
 Match length 79
 % identity 56
 NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]

Seq. No. 400138
 Seq. ID LIB3431-030-P1-N1-B8
 Method BLASTX
 NCBI GI g132105
 BLAST score 207
 E value 8.0e-23
 Match length 56
 % identity 93
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 400139
 Seq. ID LIB3431-030-P1-N1-B9
 Method BLASTX
 NCBI GI g4115536
 BLAST score 293
 E value 2.0e-26
 Match length 114

Seq. ID	LIB3431-030-P1-N1-E12
Method	BLASTX
NCBI GI	g1709620
BLAST score	178
E value	9.0e-13
Match length	55
% identity	71
NCBI Description	PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) >gi_508975 (U11496) protein disulfide isomerase [Triticum aestivum] >gi_1094851_prf_2106410A protein disulfide isomerase [Triticum aestivum]
Seq. No.	400159
Seq. ID	LIB3431-030-P1-N1-E2
Method	BLASTX
NCBI GI	g131225
BLAST score	337
E value	2.0e-31
Match length	94
% identity	70
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]
Seq. No.	400160
Seq. ID	LIB3431-030-P1-N1-E4
Method	BLASTX
NCBI GI	g347451
BLAST score	152
E value	7.0e-10
Match length	38
% identity	79
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]
Seq. No.	400161
Seq. ID	LIB3431-030-P1-N1-E6
Method	BLASTX
NCBI GI	g671740
BLAST score	512
E value	6.0e-52
Match length	94
% identity	98
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]
Seq. No.	400162
Seq. ID	LIB3431-030-P1-N1-E8
Method	BLASTX
NCBI GI	g5802606
BLAST score	498
E value	3.0e-50
Match length	104
% identity	86
NCBI Description	(AF174486) methylenetetrahydrofolate reductase [Zea mays]

E value 4.0e-49
 Match length 90
 % identity 99
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 400178
 Seq. ID LIB3431-030-P1-N1-H1
 Method BLASTN
 NCBI GI g1398998
 BLAST score 162
 E value 8.0e-86
 Match length 275
 % identity 97
 NCBI Description Rice OSOEE2 gene for 23 kDa polypeptide of photosystem II, complete cds

Seq. No. 400179
 Seq. ID LIB3431-030-P1-N1-H10
 Method BLASTN
 NCBI GI g2331130
 BLAST score 259
 E value 1.0e-144
 Match length 271
 % identity 99
 NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds

Seq. No. 400180
 Seq. ID LIB3431-030-P1-N1-H2
 Method BLASTX
 NCBI GI g3036951
 BLAST score 451
 E value 9.0e-45
 Match length 86
 % identity 99
 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 400181
 Seq. ID LIB3431-030-P1-N1-H3
 Method BLASTX
 NCBI GI g417260
 BLAST score 303
 E value 2.0e-27
 Match length 77
 % identity 74
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

Seq. No. 400182
 Seq. ID LIB3431-030-P1-N1-H6
 Method BLASTX
 NCBI GI g4079798
 BLAST score 301
 E value 2.0e-27


```
E value          4.0e-64
Match length     116
% identity       100
NCBI Description SUPEROXIDE DISMUTASE-1 [CU-ZN] >gi_280412_pir_S22508
                 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) sodA - rice
                 >gi_218224_dbj_BAA00799_ (D00999) copper/zinc-superoxide
                 dismutase [Oryza sativa] >gi_685242 (L19435) cytosolic
                 copper/zinc-superoxide dismutase [Oryza sativa]
                 >gi_1096504_prf_2111424A Cu/Zn superoxide dismutase [Oryza
                 sativa]
```

```
Seq. No.          400193
Seq. ID           LIB3431-031-P1-K1-A8
Method            BLASTX
NCBI GI           g5903036
BLAST score       316
E value           4.0e-29
Match length      132
% identity        52
NCBI Description   (AC008016) F6D8.5 [Arabidopsis thaliana]
```

Seq. No.	400194
Seq. ID	LIB3431-031-P1-K1-B1
Method	BLASTX
NCBI GI	g5702231
BLAST score	195
E value	7.0e-15
Match length	110
% identity	45
NCBI Description	(AF145386) hypersensitive reaction associated Ca2+-binding protein [Phaseolus vulgaris]

```
Seq. No.          400195
Seq. ID           LIB3431-031-P1-K1-B10
Method            BLASTX
NCBI GI           g320618
BLAST score       285
E value           5.0e-26
Match length      62
% identity        89
NCBI Description  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_(D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
```

Seq. No.	400196
Seq. ID	LIB3431-031-P1-K1-B2
Method	BLASTX
NCBI GI	g2754849
BLAST score	254
E value	7.0e-22
Match length	56
% identity	88
NCBI Description	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]


```
Seq. No.      400211
Seq. ID       LIB3431-031-P1-K1-E8
Method        BLASTX
NCBI GI       g417260
BLAST score    372
E value       1.0e-35
Match length   121
% identity     64
NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
               lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
               light-regulated gene [Oryza sativa]
```

```
Seq. No.          400212
Seq. ID           LIB3431-031-P1-K1-E9
Method            BLASTX
NCBI GI           g3914466
BLAST score       258
E value           6.0e-24
Match length      60
% identity         92
NCBI Description  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
                  (PSI-N) >gi_2981214 (AF052429) photosystem I complex Psan
                  subunit precursor [Zea mays]
```

```
Seq. No.      400213
Seq. ID       LIB3431-031-P1-K1-F1
Method        BLASTX
NCBI GI       g3913018
BLAST score   579
E value       6.0e-60
Match length  117
% identity    100
NCBI Description  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic
                aldolase [Oryza sativa]
```

```
Seq. No.      400214
Seq. ID      LIB3431-031-P1-K1-F10
Method       BLASTX
NCBI GI      g2688824
BLAST score   146
E value      3.0e-09
Match length  76
% identity    47
NCBI Description (U93273) putative auxin-repressed protein [Prunus
                  armeniaca]
```

```
Seq. No.      400215
Seq. ID      LIB3431-031-P1-K1-F11
Method       BLASTX
NCBI GI      g2944178
BLAST score   346
E value      1.0e-32
Match length  116
% identity    59
NCBI Description (AF007778) trehalose-6-phosphate phosphatase [Arabidopsis
thaliana]
```

```
Seq. No.          400216
Seq. ID           LIB3431-031-P1-K1-F12
Method            BLASTX
NCBI GI           g132105
BLAST score       559
E value           1.0e-57
Match length      122
% identity        86
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
```

```
Seq. No.      400217
Seq. ID      LIB3431-031-P1-K1-F2
Method       BLASTN
NCBI GI      g20369
BLAST score   335
E value      0.0e+00
Match length  351
% identity    99
NCBI Description  Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
synthetase (EC 6.3.1.2) (clone lambda-GS31)
>gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of
chloroplast localising glutamine synthetase
```

```
Seq. No.          400218
Seq. ID           LIB3431-031-P1-K1-F6
Method            BLASTX
NCBI GI           g1661160
BLAST score       178
E value           3.0e-13
Match length      59
% identity        71
NCBI Description   (U74295) chlorophyll a/b binding protein [Oryza sativa]
```

```
Seq. No.          400219
Seq. ID           LIB3431-031-P1-K1-F8
Method            BLASTX
NCBI GI           g4507223
BLAST score       460
E value           5.0e-46
Match length      135
% identity        71
NCBI Description   signal recognition particle receptor ('docking protein')
                   >gi_134892_sp_P08240 SRPR HUMAN SIGNAL RECOGNITION PARTICLE
                   RECEPTOR ALPHA SUBUNIT (SR-ALPHA) (DOCKING PROTEIN ALPHA)
                   (DP-ALPHA) >gi_88607_pir_A29440 signal recognition
                   particle receptor - human >gi_30866_emb_CAA29608_ (X06272)
                   docking protein [Homo sapiens]
```

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Seq. No. 400220
 Seq. ID LIB3431-031-P1-K1-F9
 Method BLASTX
 NCBI GI g82080
 BLAST score 333
 E value 4.0e-31
 Match length 104
 % identity 64
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
 >gi_226872_prf_1609235A chlorophyll a/b binding protein
 [Lycopersicon esculentum]

Seq. No. 400221
 Seq. ID LIB3431-031-P1-K1-G3
 Method BLASTX
 NCBI GI g132105
 BLAST score 600
 E value 2.0e-62
 Match length 129
 % identity 88
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 400222
 Seq. ID LIB3431-031-P1-K1-G4
 Method BLASTX
 NCBI GI g2130127
 BLAST score 397
 E value 1.0e-38
 Match length 92
 % identity 84
 NCBI Description ferritin 1 precursor - maize >gi_1103628_emb_CAA58146_
 (X83076) ferritin [Zea mays]

Seq. No. 400223
 Seq. ID LIB3431-031-P1-K1-G5
 Method BLASTX
 NCBI GI g115787
 BLAST score 614
 E value 5.0e-64
 Match length 137
 % identity 89
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
 protein 2R precursor - rice >gi_20182_emb_CAA32109_
 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
 [Oryza sativa]

Seq. No. 400224
 Seq. ID LIB3431-031-P1-K1-H11

```

Method                BLASTX
NCBI GI               g217909
BLAST score           353
E value               2.0e-33
Match length          105
% identity             69
NCBI Description      (D14044) glycolate oxidase [Cucurbita sp.]

Seq. No.              400225
Seq. ID               LIB3431-031-P1-N1-A3
Method                BLASTX
NCBI GI               g3914466
BLAST score           472
E value               2.0e-47
Match length          90
% identity             96
NCBI Description      PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
                      (PSI-N) >gi_2981214 (AF052429) photosystem I complex Psan
                      subunit precursor [Zea mays]

Seq. No.              400226
Seq. ID               LIB3431-031-P1-N1-A4
Method                BLASTX
NCBI GI               g417260
BLAST score           338
E value               2.0e-31
Match length          115
% identity             62
NCBI Description      LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
                      lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
                      light-regulated gene [Oryza sativa]

Seq. No.              400227
Seq. ID               LIB3431-031-P1-N1-A5
Method                BLASTX
NCBI GI               g671740
BLAST score           227
E value               2.0e-18
Match length          45
% identity             96
NCBI Description      (X84730) ribulose-bisphosphate carboxylase [synthetic
                      construct]

Seq. No.              400228
Seq. ID               LIB3431-031-P1-N1-A6
Method                BLASTX
NCBI GI               g4914452
BLAST score           274
E value               6.0e-24
Match length          75
% identity             68
NCBI Description      (AL050398) putative protein [Arabidopsis thaliana]

Seq. No.              400229
Seq. ID               LIB3431-031-P1-N1-A7
Method                BLASTX
NCBI GI               g538430

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09634016 103000

Seq. No.	400243
Seq. ID	LIB3431-031-P1-N1-D1
Method	BLASTN

>gi_478404_pir_JQ2247 photosystem I chain D precursor -
barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 400267
Seq. ID LIB3431-031-P1-N1-H1
Method BLASTX
NCBI GI g4886443
BLAST score 219
E value 1.0e-17
Match length 62
% identity 76
NCBI Description (AL050268) hypothetical protein [Homo sapiens]

Seq. No. 400268
Seq. ID LIB3431-031-P1-N1-H11
Method BLASTX
NCBI GI g1486472
BLAST score 168
E value 9.0e-12
Match length 33
% identity 85
NCBI Description (X99853) oxoglutarate malate translocator [Solanum tuberosum]

Seq. No. 400269
Seq. ID LIB3431-031-P1-N1-H12
Method BLASTX
NCBI GI g2570515
BLAST score 148
E value 2.0e-09
Match length 38
% identity 71
NCBI Description (AF022740) glycolate oxidase [Oryza sativa]

Seq. No. 400270
Seq. ID LIB3431-031-P1-N1-H6
Method BLASTX
NCBI GI g733454
BLAST score 446
E value 3.0e-44
Match length 91
% identity 95
NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No. 400271
Seq. ID LIB3431-031-P1-N1-H7
Method BLASTN
NCBI GI g5295987
BLAST score 124
E value 4.0e-63
Match length 359
% identity 84
NCBI Description Oryza sativa mRNA for MADS box-like protein, complete cds, clone:S10304

Seq. No. 400272

NCBI Description LHCI-680, photosystem I antenna protein - barley
>gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
antenna protein [Hordeum vulgare]

Seq. No. 400277
Seq. ID LIB3431-033-P1-K1-A4
Method BLASTX
NCBI GI g2286153
BLAST score 529
E value 4.0e-60
Match length 138
% identity 80
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No. 400278
Seq. ID LIB3431-033-P1-K1-A6
Method BLASTX
NCBI GI g1419090
BLAST score 431
E value 1.0e-42
Match length 116
% identity 72
NCBI Description (X94968) 37kDa chloroplast inner envelope membrane
polypeptide precursor [Nicotiana tabacum]

Seq. No. 400279
Seq. ID LIB3431-033-P1-K1-A7
Method BLASTX
NCBI GI g710308
BLAST score 377
E value 3.0e-36
Match length 72
% identity 94
NCBI Description (U11693) victorin binding protein [Avena sativa]

Seq. No. 400280
Seq. ID LIB3431-033-P1-K1-A8
Method BLASTX
NCBI GI g5733866
BLAST score 442
E value 8.0e-44
Match length 140
% identity 62
NCBI Description (AC007932) Contains similarity to gb_M73488
1-aminocyclopropane-1-carboxylate deaminase from
Pseudomonas sp. ESTs gb_Z18033 and gb_Z34214 come from
this gene. [Arabidopsis thaliana]

Seq. No. 400281
Seq. ID LIB3431-033-P1-K1-A9
Method BLASTN
NCBI GI g218207
BLAST score 246
E value 1.0e-136
Match length 246
% identity 100
NCBI Description Oryza sativa mRNA for the small subunit of

09694016 3 10100

```
Seq. No.      400293
Seq. ID       LIB3431-033-P1-K1-C9
Method        BLASTX
NCBI GI       g2507455
BLAST score   617
E value       2.0e-64
Match length  141
% identity    82
NCBI Description  FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE
SYNTHETASE) (FHS) (FTHFS) >gi_322401_pir_A43350
formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach
>gi_170145 (M83940) 10-formyltetrahydrofolate synthetase
[Spinacia oleracea]
```

```
Seq. No.          400294
Seq. ID           LIB3431-033-P1-K1-D1
Method            BLASTN
NCBI GI           g3789953
BLAST score       317
E value           1.0e-178
Match length      317
% identity        100
NCBI Description   Oryza sativa chlorophyll a/b-binding protein precursor
                  (Cab26) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
```

Seq. No.	400295
Seq. ID	LIB3431-033-P1-K1-D10
Method	BLASTX
NCBI GI	g3201656
BLAST score	178
E value	6.0e-13
Match length	85
% identity	47
NCBI Description	(AF005933) galactokinase [Lactobacillus casei]

51252

NCBI GI g3885888
 BLAST score 180
 E value 4.0e-13
 Match length 83
 % identity 52
 NCBI Description (AF093632) high mobility group protein [Oryza sativa]

Seq. No. 400297
 Seq. ID LIB3431-033-P1-K1-D12
 Method BLASTX
 NCBI GI g2407281
 BLAST score 674
 E value 5.0e-71
 Match length 127
 % identity 98
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 400298
 Seq. ID LIB3431-033-P1-K1-D2
 Method BLASTN
 NCBI GI g20262
 BLAST score 225
 E value 1.0e-123
 Match length 225
 % identity 100
 NCBI Description O.sativa light-induced mRNA

Seq. No. 400299
 Seq. ID LIB3431-033-P1-K1-D4
 Method BLASTX
 NCBI GI g5729802
 BLAST score 254
 E value 8.0e-22
 Match length 53
 % identity 83
 NCBI Description similar to S. pombe diml+ >gi_2565275 (AF023611) Dimlp homolog [Homo sapiens]

Seq. No. 400300
 Seq. ID LIB3431-033-P1-K1-D5
 Method BLASTX
 NCBI GI g1169798
 BLAST score 688
 E value 1.0e-72
 Match length 145
 % identity 92
 NCBI Description GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC B (GPI-B) (PHOSPHOGLUCOSE ISOMERASE B) (PGI-B) (PHOSPHOHEXOSE ISOMERASE B) (PHI-B) >gi_639686_dbj_BAA08149_ (D45218) phosphoglucose isomerase (Pgi-b) [Oryza sativa]

Seq. No. 400301
 Seq. ID LIB3431-033-P1-K1-D6
 Method BLASTX
 NCBI GI g3345477
 BLAST score 662

096406 101000

```
Seq. No.      400308
Seq. ID      LIB3431-033-P1-K1-E3
Method       BLASTX
NCBI GI      g3345477
BLAST score   630
E value      6.0e-66
Match length  135
% identity    90
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
```

```
Seq. No.          400309
Seq. ID           LIB3431-033-P1-K1-E4
Method            BLASTX
NCBI GI           g417260
BLAST score       410
E value           5.0e-40
Match length      128
% identity        65
NCBI Description   LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
                  lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
                  light-regulated gene [Oryza sativa]
```

```
Seq. No.      400310
Seq. ID      LIB3431-033-P1-K1-E5
Method       BLASTX
NCBI GI      g115787
BLAST score   376
E value      4.0e-36
Match length  73
% identity    99
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
```

51255

NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA14-A >gi_167326
(M88321) Group 4 late embryogenesis-abundant protein
[Gossypium hirsutum] >gi_167328 (M88322) Group 4 late
embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 400336
Seq. ID LIB3431-033-P1-K1-H2
Method BLASTX
NCBI GI g2570511
BLAST score 580
E value 4.0e-60
Match length 111
% identity 98
NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No. 400337
Seq. ID LIB3431-033-P1-K1-H4
Method BLASTN
NCBI GI g2072554
BLAST score 173
E value 1.0e-92
Match length 249
% identity 92
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
cds

Seq. No. 400338
Seq. ID LIB3431-033-P1-K1-H7
Method BLASTX
NCBI GI g132105
BLAST score 582
E value 3.0e-60
Match length 125
% identity 87
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 400339
Seq. ID LIB3431-033-P1-K1-H9
Method BLASTX
NCBI GI g170131
BLAST score 383
E value 6.0e-37
Match length 98
% identity 71
NCBI Description (M55322) ribosomal protein 30S subunit [Spinacia oleracea]

Seq. No. 400340
Seq. ID LIB3431-033-P1-N1-A1
Method BLASTX

```

NCBI GI             g3789948
BLAST score         167
E value             1.0e-11
Match length        34
% identity           97
NCBI Description     (AF094773) translation initiation factor 5A [Oryza sativa]

```

```
Seq. No.      400341
Seq. ID      LIB3431-033-P1-N1-A11
Method       BLASTX
NCBI GI      g115784
BLAST score   145
E value      4.0e-09
Match length  26
% identity    100
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I (CAB)
                  (LHCP) >gi_167525 (M16058) chlorophyll a/b-binding protein
                  [Cucumis sativus]
```

```
Seq. No.          400342
Seq. ID          LIB3431-033-P1-N1-A12
Method          BLASTX
NCBI GI         g548603
BLAST score      294
E value         1.0e-26
Match length     57
% identity       96
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
                 (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                 >gi_478404_pir_JQ2247 photosystem I chain D precursor -
                 barley >qi_167085 (M98254) PSI-D subunit [Hordeum vulgare]
```

Seq. No.	400343
Seq. ID	LIB3431-033-P1-N1-A3
Method	BLASTN
NCBI GI	g2306980
BLAST score	229
E value	1.0e-126
Match length	254
% identity	98
NCBI Description	Oryza sativa photosystem I antenna protein (Lhca) mRNA, complete cds

```
Seq. No.      400344
Seq. ID      LIB3431-033-P1-N1-A4
Method       BLASTX
NCBI GI      g2286153
BLAST score   249
E value      2.0e-21
Match length  50
% identity    94
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
```

```
Seq. No.      400345
Seq. ID       LIB3431-033-P1-N1-A5
Method        BLASTN
NCBI GI       q2570514
```


009684015-101000

Seq. No. 400356
Seq. ID LIB3431-033-P1-N1-C6
Method BLASTN
NCBI GI g5091597
BLAST score 33
E value 4.0e-09
Match length 45
% identity 93
NCBI Description Oryza sativa chromosome 1 BAC 10A19I, complete sequence.

Seq. No. 400357
Seq. ID LIB3431-033-P1-N1-C7
Method BLASTX
NCBI GI g482311
BLAST score 171
E value 3.0e-12
Match length 33
% identity 100
NCBI Description photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No. 400358
Seq. ID LIB3431-033-P1-N1-C8
Method BLASTX
NCBI GI g482311
BLAST score 315
E value 5.0e-29
Match length 63
% identity 100
NCBI Description photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No. 400359
Seq. ID LIB3431-033-P1-N1-D1
Method BLASTN
NCBI GI g3789953
BLAST score 317
E value 1.0e-178
Match length 317
% identity 100
NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor (Cab26) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 400360
Seq. ID LIB3431-033-P1-N1-D11
Method BLASTN
NCBI GI g3885887
BLAST score 297
E value 1.0e-166
Match length 301
% identity 100
NCBI Description Oryza sativa high mobility group protein (HMG) mRNA, complete cds

Seq. ID	LIB3431-033-P1-N1-G1
Method	BLASTN
NCBI GI	g2662309
BLAST score	53
E value	8.0e-21
Match length	61
% identity	97
NCBI Description	Hordeum vulgare mRNA for bpw1, complete cds

```
Seq. No.      400381
Seq. ID      LIB3431-033-P1-N1-G11
Method       BLASTX
NCBI GI      g2326947
BLAST score   231
E value      4.0e-19
Match length  44
% identity    100
NCBI Description (Z50801) Chlorophyll a/b-binding protein CP29 precursor
               [Zea mays]
```

Seq. No.	400382
Seq. ID	LIB3431-033-P1-N1-G2
Method	BLASTN
NCBI GI	g4079797
BLAST score	129
E value	3.0e-66
Match length	251
% identity	100
NCBI Description	Oryza sativa 23 kDa polypeptide of photosystem II mRNA, complete cds

```
Seq. No.          400383
Seq. ID           LIB3431-033-P1-N1-G3
Method            BLASTX
NCBI GI           g1076724
BLAST score       268
E value           2.0e-23
Match length      52
% identity         96
NCBI Description   LHCI-680, photosystem I antenna protein - barley
                   >gi_666054_emb_CAA59049_(X84308) LHCI-680, photosystem I
                   antenna protein [Hordeum vulgare]
```

```
Seq. No.      400384
Seq. ID      LIB3431-033-P1-N1-G4
Method       BLASTX
NCBI GI      g2673917
BLAST score   154
E value      4.0e-10
Match length  43
% identity    65
NCBI Description (AC002561) putative ATP-dependent RNA helicase [Arabidopsis thaliana]
```

Seq. No.	400385
Seq. ID	LIB3431-033-P1-N1-G6
Method	BLASTX

0000016-101000

NCBI GI g1710551
BLAST score 248
E value 4.0e-21
Match length 46
% identity 98
NCBI Description 60S RIBOSOMAL PROTEIN L39 >gi_1177369_emb_CAA64728.1_
(X95458) ribosomal protein L39 [Zea mays]

Seq. No. 400386
Seq. ID LIB3431-033-P1-N1-G7
Method BLASTN
NCBI GI g2073379
BLAST score 88
E value 8.0e-42
Match length 88
% identity 100
NCBI Description Rice CP26 mRNA, partial sequence

Seq. No. 400387
Seq. ID LIB3431-033-P1-N1-G9
Method BLASTX
NCBI GI g586339
BLAST score 207
E value 3.0e-16
Match length 71
% identity 51
NCBI Description PEROXISOMAL-COENZYME A SYNTHETASE >gi_626794_pir_S46098
probable AMP-binding protein - yeast (Saccharomyces
cerevisiae) >gi_536615_emb_CAA85185_ (Z36091) ORF YBR222c
[Saccharomyces cerevisiae]

Seq. No. 400388
Seq. ID LIB3431-033-P1-N1-H10
Method BLASTX
NCBI GI g1617197
BLAST score 152
E value 6.0e-10
Match length 30
% identity 90
NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 400389
Seq. ID LIB3431-033-P1-N1-H12
Method BLASTX
NCBI GI g1170745
BLAST score 331
E value 2.0e-33
Match length 103
% identity 67
NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA14-A >gi_167326
(M88321) Group 4 late embryogenesis-abundant protein
[Gossypium hirsutum] >gi_167328 (M88322) Group 4 late
embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 400390
Seq. ID LIB3431-033-P1-N1-H2
Method BLASTX

NCBI GI	g4689380
BLAST score	258
E value	3.0e-22
Match length	52
% identity	94
NCBI Description	(AF139465) LHCII type III chlorophyll a/b binding protein [Vigna radiata]

Seq. No.	400391
Seq. ID	LIB3431-033-P1-N1-H4
Method	BLASTN
NCBI GI	g2072554
BLAST score	290
E value	1.0e-162
Match length	294
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

```

Seq. No.      400392
Seq. ID       LIB3431-033-P1-N1-H7
Method        BLASTX
NCBI GI       g132105
BLAST score   301
E value       2.0e-27
Match length  57
% identity    100
NCBI Description  RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]

```

```
Seq. No.      400393
Seq. ID      LIB3431-033-P1-N1-H9
Method       BLASTX
NCBI GI      g170131
BLAST score   152
E value      6.0e-10
Match length  47
% identity    64
NCBI Description (M55322) ribosomal protein 30S subunit [Spinacia oleracea]
```

Seq. No.	400394
Seq. ID	LIB3431-034-P1-K1-A11
Method	BLASTX
NCBI GI	g4469021
BLAST score	268
E value	2.0e-23
Match length	78
% identity	69
NCBI Description	(AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No.	400395
Seq. ID	LIB3431-034-P1-K1-A12
Method	BLASTX
NCBI GI	g1835731
BLAST score	310
E value	2.0e-28
Match length	71
% identity	83
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

```
Seq. No.          400396
Seq. ID           LIB3431-034-P1-K1-A2
Method            BLASTX
NCBI GI           g548605
BLAST score       522
E value           3.0e-53
Match length      114
% identity        91
NCBI Description  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi_539055_pir_A48527 photosystem I protein psaK precursor
                  - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
```

Seq. No.	400397
Seq. ID	LIB3431-034-P1-K1-A3
Method	BLASTX
NCBI GI	g3080375
BLAST score	386
E value	3.0e-37
Match length	118
% identity	64
NCBI Description	(AL022580) putative protein [Arabidopsis thaliana]

```
Seq. No.          400398
Seq. ID           LIB3431-034-P1-K1-A4
Method            BLASTN
NCBI GI           g6015437
BLAST score       36
E value           1.0e-10
Match length      47
% identity        65
NCBI Description   Homo sapiens PEX1 mRNA, complete cds
```

```
Seq. No.      400399
Seq. ID       LIB3431-034-P1-K1-A6
Method        BLASTX
NCBI GI       g3420055
BLAST score   294
E value       2.0e-26
Match length  62
% identity    89
NCBI Description (AC004680) cyclophilin [Arabidopsis thaliana]
```

```
Seq. No.      400400
Seq. ID      LIB3431-034-P1-K1-A7
Method       BLASTN
```


Seq. No. 400410
 Seq. ID LIB3431-034-P1-K1-B7
 Method BLASTX
 NCBI GI g4587571
 BLAST score 148
 E value 2.0e-15
 Match length 82
 % identity 56
 NCBI Description (AC006550) Belongs to the PF_01027 Uncharacterized protein family UPF0005 with 7 transmembrane domains. [Arabidopsis thaliana]

Seq. No. 400411
 Seq. ID LIB3431-034-P1-K1-B9
 Method BLASTX
 NCBI GI g2492514
 BLAST score 672
 E value 7.0e-71
 Match length 141
 % identity 94
 NCBI Description CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
 >gi_1483215_emb_CAA68141_ (X99808) chloroplast FtsH protease [Arabidopsis thaliana]

Seq. No. 400412
 Seq. ID LIB3431-034-P1-K1-C11
 Method BLASTX
 NCBI GI g5091509
 BLAST score 509
 E value 7.0e-52
 Match length 115
 % identity 88
 NCBI Description (AB023482) EST AU065533(C2174) corresponds to a region of the predicted gene.; Similar to Homo sapiens splicing factor Prp8 mRNA, complete cds. (AF092565) [Oryza sativa]

Seq. No. 400413
 Seq. ID LIB3431-034-P1-K1-C4
 Method BLASTX
 NCBI GI g464705
 BLAST score 594
 E value 1.0e-61
 Match length 122
 % identity 97
 NCBI Description 40S RIBOSOMAL PROTEIN S13 >gi_419802_pir_S30146 ribosomal protein S13.e - maize >gi_288059_emb_CAA44311_ (X62455) cytoplasmatic ribosomal protein S13 [Zea mays]

Seq. No. 400414
 Seq. ID LIB3431-034-P1-K1-D10
 Method BLASTN
 NCBI GI g218218
 BLAST score 67
 E value 4.0e-29
 Match length 95
 % identity 93
 NCBI Description Oryza sativa p-SINE1-r3 gene, repeat sequence

NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

```
Seq. No.      400420
Seq. ID      LIB3431-034-P1-K1-D6
Method       BLASTX
NCBI GI      g461899
BLAST score   506
E value      2.0e-51
```

NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST PRECURSOR (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_1076368_pir_B53422 peptidylprolyl isomerase (EC 5.2.1.8) ROC4 - *Arabidopsis thaliana* >gi_405131 (L14845) cyclophilin [*Arabidopsis thaliana*] >gi_1322278 (U42724) cyclophilin [*Arabidopsis thaliana*]

```
Seq. No.          400421
Seq. ID           LIB3431-034-P1-K1-D7
Method            BLASTX
NCBI GI           g115787
BLAST score       535
E value           9.0e-55
Match length      122
% identity        88
```

```
Seq. No.      400422
Seq. ID      LIB3431-034-P1-K1-D9
Method       BLASTX
NCBI GI      g132105
BLAST score   481
E value      2.0e-48
Match length  109
% identity    85
NCBI Description RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                (D00643) small subunit of ribulose-1,5-bisphosphate
                carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                carboxylase S [Oryza sativa]
```

```
Seq. No.      400423
Seq. ID      LIB3431-034-P1-K1-E10
Method       BLASTX
NCBI GI      g320618
BLAST score   551
E value      1.0e-56
Match length 120
```


000T0T-9T048960

% identity 56
NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 400429
Seq. ID LIB3431-034-P1-K1-E7
Method BLASTX
NCBI GI g2104959
BLAST score 188
E value 4.0e-14
Match length 42
% identity 81
NCBI Description (U96925) immunophilin [Vicia faba]

Seq. No. 400430
Seq. ID LIB3431-034-P1-K1-E9
Method BLASTN
NCBI GI g218171
BLAST score 159
E value 4.0e-84
Match length 279
% identity 89
NCBI Description Oryza sativa mRNA for type I light-harvesting chlorophyll a/b binding protein of photosystem II (LHCPII), complete cds

Seq. No. 400431
Seq. ID LIB3431-034-P1-K1-F1
Method BLASTX
NCBI GI g320618
BLAST score 435
E value 4.0e-43
Match length 89
% identity 94
NCBI Description chlorophyll a/b-binding protein I precursor - rice
>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa]
>gi_227611_prf_1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No. 400432
Seq. ID LIB3431-034-P1-K1-F11
Method BLASTX
NCBI GI g3913018
BLAST score 723
E value 8.0e-77
Match length 139
% identity 99
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]

Seq. No. 400433
Seq. ID LIB3431-034-P1-K1-F12
Method BLASTX
NCBI GI g283971
BLAST score 365
E value 8.0e-35

Match length 137
 % identity 51
 NCBI Description aldehyde dehydrogenase (NAD(P)+) (EC 1.2.1.5) 3 - human
 >gi_178375 (M77477) aldehyde dehydrogenase [Homo sapiens]
 >gi_300402_bbs_132241 (S61044) aldehyde dehydrogenase
 isozyme 3, ALDH3 {EC 1.2.1.3} [human, stomach, Peptide, 453
 aa] [Homo sapiens]

Seq. No. 400434
 Seq. ID LIB3431-034-P1-K1-F2
 Method BLASTX
 NCBI GI g6013233
 BLAST score 301
 E value 3.0e-27
 Match length 140
 % identity 41
 NCBI Description (AF183932) ionotropic glutamate receptor homolog
 [Arabidopsis thaliana]

Seq. No. 400435
 Seq. ID LIB3431-034-P1-K1-F4
 Method BLASTX
 NCBI GI g3126854
 BLAST score 675
 E value 4.0e-71
 Match length 127
 % identity 100
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 400436
 Seq. ID LIB3431-034-P1-K1-F5
 Method BLASTX
 NCBI GI g115794
 BLAST score 218
 E value 1.0e-17
 Match length 78
 % identity 60
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
 III CAB-13) >gi_72748_pir_CDT033 chlorophyll a/b-binding
 protein type III precursor (cab-13) - tomato
 >gi_19277_emb_CAA42818_ (X60275) LHCII type III
 [Lycopersicon esculentum]

Seq. No. 400437
 Seq. ID LIB3431-034-P1-K1-F6
 Method BLASTX
 NCBI GI g6006363
 BLAST score 271
 E value 7.0e-24
 Match length 51
 % identity 100
 NCBI Description (AP000559) ESTs AU078183(C62904),C73912(E21020) correspond
 to a region of the predicted gene.; Similar to water stress
 inducible protein (U74296) [Oryza sativa]

Seq. No. 400438
 Seq. ID LIB3431-034-P1-K1-F7

Match length 66
 % identity 47
 NCBI Description (AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 400449
 Seq. ID LIB3431-034-P1-K1-H11
 Method BLASTX
 NCBI GI g548605
 BLAST score 594
 E value 1.0e-61
 Match length 130
 % identity 91
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
 (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
 >gi_539055_pir_A48527 photosystem I protein psaK precursor
 - barley >gi_304220 (L12707) photosystem I PSI-K subunit
 [Hordeum vulgare]

Seq. No. 400450
 Seq. ID LIB3431-034-P1-K1-H3
 Method BLASTX
 NCBI GI g417482
 BLAST score 397
 E value 1.0e-38
 Match length 140
 % identity 58
 NCBI Description PROTEIN FARNESYLTRANSFERASE BETA SUBUNIT (CAAX
 FARNESYLTRANSFERASE BETA SUBUNIT) (RAS PROTEINS
 PRENYLTRANSFERASE) (FTASE-BETA) >gi_541966_pir_JQ2254
 farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) beta
 chain - garden pea >gi_169049 (L08664) farnesyl-protein
 transferase beta-subunit [Pisum sativum]

Seq. No. 400451
 Seq. ID LIB3431-034-P1-K1-H5
 Method BLASTX
 NCBI GI g6006429
 BLAST score 298
 E value 6.0e-27
 Match length 118
 % identity 49
 NCBI Description (AJ242958) SPL1-Related3 protein [Arabidopsis thaliana]

Seq. No. 400452
 Seq. ID LIB3431-034-P1-K1-H7
 Method BLASTX
 NCBI GI g132105
 BLAST score 547
 E value 4.0e-56
 Match length 119
 % identity 87
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)

0001015-101000

000101"9T0B960

ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 400453
Seq. ID LIB3431-034-P1-K1-H9
Method BLASTN
NCBI GI g2073379
BLAST score 88
E value 5.0e-42
Match length 92
% identity 99
NCBI Description Rice CP26 mRNA, partial sequence

Seq. No. 400454
Seq. ID LIB3431-034-P1-N1-A11
Method BLASTX
NCBI GI g4469021
BLAST score 292
E value 4.0e-26
Match length 76
% identity 74
NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No. 400455
Seq. ID LIB3431-034-P1-N1-A12
Method BLASTX
NCBI GI g1835731
BLAST score 273
E value 4.0e-24
Match length 65
% identity 82
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 400456
Seq. ID LIB3431-034-P1-N1-A2
Method BLASTN
NCBI GI g304219
BLAST score 49
E value 1.0e-18
Match length 71
% identity 92
NCBI Description Hordeum vulgare chloroplast photosystem I PSK-I subunit mRNA, complete cds

Seq. No. 400457
Seq. ID LIB3431-034-P1-N1-A6
Method BLASTX
NCBI GI g3420055
BLAST score 260
E value 2.0e-22
Match length 55
% identity 89
NCBI Description (AC004680) cyclophilin [Arabidopsis thaliana]

Seq. No. 400458
Seq. ID LIB3431-034-P1-N1-A8

0001016-101000

Method BLASTX
 NCBI GI g3914899
 BLAST score 199
 E value 2.0e-15
 Match length 41
 % identity 93
 NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi_2331301 (AF013487) ribosomal protein S4 type I [Zea mays]

Seq. No. 400459
 Seq. ID LIB3431-034-P1-N1-B10
 Method BLASTX
 NCBI GI g3036951
 BLAST score 356
 E value 8.0e-34
 Match length 68
 % identity 100
 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 400460
 Seq. ID LIB3431-034-P1-N1-B2
 Method BLASTN
 NCBI GI g4079797
 BLAST score 92
 E value 2.0e-44
 Match length 163
 % identity 98
 NCBI Description Oryza sativa 23 kDa polypeptide of photosystem II mRNA, complete cds

Seq. No. 400461
 Seq. ID LIB3431-034-P1-N1-B3
 Method BLASTN
 NCBI GI g218180
 BLAST score 294
 E value 1.0e-164
 Match length 390
 % identity 93
 NCBI Description Rice mRNA for oryzain alpha (EC 3.4.22)

Seq. No. 400462
 Seq. ID LIB3431-034-P1-N1-B5
 Method BLASTN
 NCBI GI g1815627
 BLAST score 116
 E value 3.0e-58
 Match length 151
 % identity 97
 NCBI Description Oryza sativa metallothionein-like type 2 (OsMT-2) mRNA, complete cds

Seq. No. 400463
 Seq. ID LIB3431-034-P1-N1-B6
 Method BLASTX
 NCBI GI g480450
 BLAST score 542

```
E value      2.0e-55
Match length 150
% identity   74
NCBI Description ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
thaliana >gi_402552_emb_CAA49506_(X69880) ketol-acid
reductoisomerase [Arabidopsis thaliana]
```

```
Seq. No.      400464
Seq. ID       LIB3431-034-P1-N1-B9
Method        BLASTX
NCBI GI       g5734790
BLAST score    337
E value        1.0e-31
Match length   74
% identity     89
NCBI Description (AC007980) ATP-dependent metalloprotease [Arabidopsis thaliana]
```

```
Seq. No.      400465
Seq. ID      LIB3431-034-P1-N1-C1
Method       BLASTN
NCBI GI      g3789951
BLAST score   96
E value      1.0e-46
Match length  211
% identity    86
NCBI Description  Oryza sativa chlorophyll a/b-binding protein presursor
                  (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
```

```
Seq. No.      400466
Seq. ID       LIB3431-034-P1-N1-C10
Method        BLASTX
NCBI GI       g671740
BLAST score   431
E value       1.0e-42
Match length  79
% identity    99
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
construct]
```

```
Seq. No.      400467
Seq. ID      LIB3431-034-P1-N1-C11
Method       BLASTX
NCBI GI      g5091509
BLAST score   262
E value      8.0e-23
Match length  47
% identity    100
NCBI Description (AB023482) EST AU065533(C2174) corresponds to a region of
the predicted gene.; Similar to Homo sapiens splicing
factor Prp8 mRNA, complete cds.(AF092565) [Oryza sativa]
```

Seq. No. 400468
Seq. ID LIB3431-034-P1-N1-C3
Method BLASTX
NCBI GI q3123295

BLAST score 231
E value 4.0e-19
Match length 57
% identity 70
NCBI Description CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED >gi_2583169
(AF026473) calmodulin-related protein [Arabidopsis
thaliana]

Seq. No. 400469
Seq. ID LIB3431-034-P1-N1-C5
Method BLASTX
NCBI GI g1296955
BLAST score 300
E value 3.0e-27
Match length 54
% identity 46
NCBI Description (X95402) duplicated domain structure protein [Oryza sativa]

Seq. No. 400470
Seq. ID LIB3431-034-P1-N1-C7
Method BLASTN
NCBI GI g1661159
BLAST score 157
E value 5.0e-83
Match length 237
% identity 92
NCBI Description Oryza sativa chlorophyll a/b binding protein (kcd1895)
mRNA, complete cds

Seq. No. 400471
Seq. ID LIB3431-034-P1-N1-C8
Method BLASTN
NCBI GI g2072726
BLAST score 461
E value 0.0e+00
Match length 503
% identity 98
NCBI Description O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2

Seq. No. 400472
Seq. ID LIB3431-034-P1-N1-C9
Method BLASTX
NCBI GI g3345477
BLAST score 211
E value 9.0e-17
Match length 44
% identity 91
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 400473
Seq. ID LIB3431-034-P1-N1-D10
Method BLASTN
NCBI GI g218218
BLAST score 85
E value 6.0e-40
Match length 112
% identity 95

NCBI Description Oryza sativa p-SINE1-r3 gene, repeat sequence

```

Seq. No.          400474
Seq. ID           LIB3431-034-P1-N1-D11
Method            BLASTX
NCBI GI           g132105
BLAST score       451
E value           6.0e-45
Match length      93
% identity        89
NCBI Description   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose biphosphate
                  carboxylase S [Oryza sativa]

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```
Seq. No.      400476
Seq. ID      LIB3431-034-P1-N1-D3
Method       BLASTX
NCBI GI      g3786007
BLAST score   160
E value      7.0e-11
Match length  43
% identity    53
NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]
```

Seq. No.	400478
Seq. ID	LIB3431-034-P1-N1-D6
Method	BLASTX
NCBI GI	q992633

09634016.101000

Match length 279
% identity 98
NCBI Description Oryza sativa chlorophyll a-b binding protein mRNA, complete cds

Seq. No. 400494
Seq. ID LIB3431-034-P1-N1-F6
Method BLASTN
NCBI GI g6006355
BLAST score 374
E value 0.0e+00
Match length 380
% identity 99
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No. 400495
Seq. ID LIB3431-034-P1-N1-F7
Method BLASTX
NCBI GI g115813
BLAST score 215
E value 3.0e-17
Match length 48
% identity 85
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_(X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 400496
Seq. ID LIB3431-034-P1-N1-F8
Method BLASTN
NCBI GI g304219
BLAST score 40
E value 3.0e-13
Match length 68
% identity 90
NCBI Description Hordeum vulgare chloroplast photosystem I PSK-I subunit mRNA, complete cds

Seq. No. 400497
Seq. ID LIB3431-034-P1-N1-F9
Method BLASTX
NCBI GI g733456
BLAST score 371
E value 2.0e-35
Match length 76
% identity 95
NCBI Description (U23189) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No. 400498
Seq. ID LIB3431-034-P1-N1-G11
Method BLASTN
NCBI GI g218209
BLAST score 149
E value 4.0e-78
Match length 328
% identity 97

% identity 75
 NCBI Description PROTEIN FARNESYLTRANSFERASE BETA SUBUNIT (CAAX
 FARNESYLTRANSFERASE BETA SUBUNIT) (RAS PROTEINS
 PRENYLTRANSFERASE) (FTASE-BETA) >gi_541966_pir_JQ2254
 farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) beta
 chain - garden pea >gi_169049 (L08664) farnesyl-protein
 transferase beta-subunit [Pisum sativum]

Seq. No. 400504
 Seq. ID LIB3431-034-P1-N1-H4
 Method BLASTN
 NCBI GI g3819197
 BLAST score 47
 E value 4.0e-17
 Match length 103
 % identity 86
 NCBI Description Hordeum vulgare partial mRNA; clone cMWG0676.uni

Seq. No. 400505
 Seq. ID LIB3431-034-P1-N1-H7
 Method BLASTN
 NCBI GI g218207
 BLAST score 295
 E value 1.0e-165
 Match length 307
 % identity 99
 NCBI Description Oryza sativa mRNA for the small subunit of
 ribulose-1,5-bisphosphate carboxylase, complete cds, clone
 pOSSS1139

Seq. No. 400506
 Seq. ID LIB3431-035-P1-K1-A1
 Method BLASTX
 NCBI GI g548605
 BLAST score 471
 E value 3.0e-47
 Match length 98
 % identity 93
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
 (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
 >gi_539055_pir_A48527 photosystem I protein psaK precursor
 - barley >gi_304220 (L12707) photosystem I PSI-K subunit
 [Hordeum vulgare]

Seq. No. 400507
 Seq. ID LIB3431-035-P1-K1-A12
 Method BLASTX
 NCBI GI g1171579
 BLAST score 239
 E value 5.0e-20
 Match length 91
 % identity 48
 NCBI Description (X95342) cytochrome P450 [Nicotiana tabacum]

Seq. No. 400508
 Seq. ID LIB3431-035-P1-K1-A2
 Method BLASTX

NCBI GI g2582822
 BLAST score 172
 E value 3.0e-12
 Match length 39
 % identity 82
 NCBI Description (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) .[Solanum tuberosum]

Seq. No. 400509
 Seq. ID LIB3431-035-P1-K1-A3
 Method BLASTX
 NCBI GI g728744
 BLAST score 271
 E value 2.0e-46
 Match length 132
 % identity 80
 NCBI Description AUXIN-INDUCED PROTEIN PCNT115 >gi_100305_pir__S16390
 auxin-induced protein - common tobacco
 >gi_19799_emb_CAA39708_ (X56267) auxin-induced protein
 [Nicotiana tabacum]

Seq. No. 400510
 Seq. ID LIB3431-035-P1-K1-A7
 Method BLASTX
 NCBI GI g5912299
 BLAST score 464
 E value 8.0e-55
 Match length 123
 % identity 88
 NCBI Description (AJ133787) gigantea homologue [Oryza sativa]

Seq. No. 400511
 Seq. ID LIB3431-035-P1-K1-B11
 Method BLASTX
 NCBI GI g1076724
 BLAST score 665
 E value 6.0e-70
 Match length 141
 % identity 85
 NCBI Description LHCI-680, photosystem I antenna protein - barley
 >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
 antenna protein [Hordeum vulgare]

Seq. No. 400512
 Seq. ID LIB3431-035-P1-K1-B3
 Method BLASTX
 NCBI GI g320618
 BLAST score 578
 E value 1.0e-59
 Match length 127
 % identity 87
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

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Seq. No. 400513
Seq. ID LIB3431-035-P1-K1-B4
Method BLASTX
NCBI GI g3386621
BLAST score 513
E value 4.0e-52
Match length 119
% identity 83
NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 400514
Seq. ID LIB3431-035-P1-K1-B5
Method BLASTX
NCBI GI g3273202
BLAST score 394
E value 4.0e-38
Match length 115
% identity 74
NCBI Description (AB010918) response reactor4 [Arabidopsis thaliana]

Seq. No. 400515
Seq. ID LIB3431-035-P1-K1-B7
Method BLASTN
NCBI GI g20181
BLAST score 92
E value 6.0e-44
Match length 243
% identity 86
NCBI Description Rice cab2R gene for light harvesting chlorophyll
a/b-binding protein

Seq. No. 400516
Seq. ID LIB3431-035-P1-K1-B8
Method BLASTX
NCBI GI g417488
BLAST score 608
E value 3.0e-63
Match length 152
% identity 75
NCBI Description ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE
H) >gi_100452_pir_A40995 starch phosphorylase (EC 2.4.1.1)
H - potato >gi_169473 (M69038) alpha-glucan phosphorylase
type H isozyme [Solanum tuberosum]

Seq. No. 400517
Seq. ID LIB3431-035-P1-K1-B9
Method BLASTX
NCBI GI g115787
BLAST score 600
E value 3.0e-62
Match length 135
% identity 88
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
protein 2R precursor - rice >gi_20182_emb_CAA32109
(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
[Oryza sativa]

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Seq. No. 400518
 Seq. ID LIB3431-035-P1-K1-C11
 Method BLASTX
 NCBI GI g2407281
 BLAST score 758
 E value 7.0e-81
 Match length 149
 % identity 95
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 400519
 Seq. ID LIB3431-035-P1-K1-C2
 Method BLASTX
 NCBI GI g100454
 BLAST score 664
 E value 7.0e-70
 Match length 146
 % identity 86
 NCBI Description photosystem II oxygen-evolving complex protein 1 - potato >gi_809113_emb_CAA35601_ (X17578) 33kDa precursor protein of oxygen-evolving complex [Solanum tuberosum]

Seq. No. 400520
 Seq. ID LIB3431-035-P1-K1-C3
 Method BLASTX
 NCBI GI g544437
 BLAST score 339
 E value 1.0e-31
 Match length 73
 % identity 86
 NCBI Description GLUTATHIONE PEROXIDASE HOMOLOG (SALT-ASSOCIATED PROTEIN) >gi_296358_emb_CAA47018_ (X66377) CIT-SAP [Citrus sinensis]

Seq. No. 400521
 Seq. ID LIB3431-035-P1-K1-C4
 Method BLASTN
 NCBI GI g473980
 BLAST score 76
 E value 9.0e-35
 Match length 113
 % identity 90
 NCBI Description Rice mRNA, partial homologous to glycine-rich protein gene

Seq. No. 400522
 Seq. ID LIB3431-035-P1-K1-C6
 Method BLASTX
 NCBI GI g82080
 BLAST score 415
 E value 1.0e-40
 Match length 141
 % identity 62
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf_1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No. 400523
 Seq. ID LIB3431-035-P1-K1-C7
 Method BLASTX
 NCBI GI g3345477
 BLAST score 662
 E value 1.0e-69
 Match length 127
 % identity 98
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 400524
 Seq. ID LIB3431-035-P1-K1-C8
 Method BLASTX
 NCBI GI g5042462
 BLAST score 450
 E value 9.0e-45
 Match length 114
 % identity 80
 NCBI Description (AC007789) putative negatively light-regulated protein [Oryza sativa]

Seq. No. 400525
 Seq. ID LIB3431-035-P1-K1-C9
 Method BLASTX
 NCBI GI g132105
 BLAST score 676
 E value 3.0e-71
 Match length 144
 % identity 89
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 400526
 Seq. ID LIB3431-035-P1-K1-D1
 Method BLASTX
 NCBI GI g1173347
 BLAST score 793
 E value 6.0e-85
 Match length 153
 % identity 95
 NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]

Seq. No. 400527
 Seq. ID LIB3431-035-P1-K1-D10
 Method BLASTX

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% identity      80
NCBI Description (U49387) adenylosuccinate synthetase [Triticum aestivum]

Seq. No.        400557
Seq. ID         LIB3431-035-P1-K1-G5
Method          BLASTX
NCBI GI         g5031281
BLAST score     314
E value         9.0e-29
Match length    98
% identity      62
NCBI Description (AF139499) unknown [Prunus armeniaca]

Seq. No.        400558
Seq. ID         LIB3431-035-P1-K1-G6
Method          BLASTN
NCBI GI         g1245938
BLAST score     35
E value         6.0e-10
Match length    35
% identity      100
NCBI Description rabClC-2 beta=chloride channel ClC-2G isoform [rabbits,
heart atrium, mRNA, 2998 nt]

Seq. No.        400559
Seq. ID         LIB3431-035-P1-K1-G8
Method          BLASTX
NCBI GI         g3885888
BLAST score     347
E value         1.0e-32
Match length    70
% identity      97
NCBI Description (AF093632) high mobility group protein [Oryza sativa]

Seq. No.        400560
Seq. ID         LIB3431-035-P1-K1-G9
Method          BLASTX
NCBI GI         g422029
BLAST score     542
E value         2.0e-55
Match length    150
% identity      73
NCBI Description transcription factor OBF3.2, ocs element-binding - maize
>gi_297018_emb_CAA48904_ (X69152) ocs-element binding
factor 3.2 [Zea mays]

Seq. No.        400561
Seq. ID         LIB3431-035-P1-K1-H1
Method          BLASTX
NCBI GI         g2407281
BLAST score     705
E value         1.0e-74
Match length    132
% identity      99
NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
subunit [Oryza sativa]
```



```

Seq. No.          400562
Seq. ID           LIB3431-035-P1-K1-H10
Method            BLASTX
NCBI GI           g132105
BLAST score       595
E value           9.0e-62
Match length      128
% identity         88
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]

```

```
Seq. No.      400563
Seq. ID       LIB3431-035-P1-K1-H11
Method        BLASTX
NCBI GI       g3914603
BLAST score    699
E value        5.0e-74
Match length   134
% identity     99
NCBI Description RIBULOSE BIPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414
                (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                activase [Oryza sativa]
```

```
Seq. No.      400564
Seq. ID      LIB3431-035-P1-K1-H12
Method       BLASTX
NCBI GI      g6063542
BLAST score   351
E value      2.0e-33
Match length  109
% identity    72
NCBI Description (AP000615) EST C74302(E30840) corresponds to a region of
the predicted gene.; similar to glyceraldehyde-3-phosphate
dehydrogenase. (M64118) [Oryza sativa]
```

```
Seq. No.      400565
Seq. ID      LIB3431-035-P1-K1-H2
Method       BLASTX
NCBI GI      g1172813
BLAST score   563
E value      5.0e-58
Match length 108
% identity   99
NCBI Description 60S RIBOSOMAL PROTEIN L10-2 (PUTATIVE TUMOR SUPPRESSOR SG12)
>gi_1076752_pir_S49596 ribosomal protein L10.e, cytosolic
- rice >gi_575357_emb_CAA57340_ (X81692) putative tumor
suppressor [Oryza sativa]
```

Seq. No. 400566

NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]
Seq. No.	400576
Seq. ID	LIB3431-035-P1-N1-C2
Method	BLASTX
NCBI GI	g482311
BLAST score	171
E value	4.0e-12
Match length	33
% identity	100
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]
Seq. No.	400577
Seq. ID	LIB3431-035-P1-N1-C3
Method	BLASTX
NCBI GI	g1362150
BLAST score	290
E value	1.0e-33
Match length	84
% identity	88
NCBI Description	hypothetical protein (clone AFN3) - wild oat (fragment) >gi_726478 (U20000) putative ORF1 [Avena fatua]
Seq. No.	400578
Seq. ID	LIB3431-035-P1-N1-C4
Method	BLASTN
NCBI GI	g2331130
BLAST score	227
E value	1.0e-125
Match length	251
% identity	98
NCBI Description	Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds
Seq. No.	400579
Seq. ID	LIB3431-035-P1-N1-C7
Method	BLASTN
NCBI GI	g218209
BLAST score	57
E value	3.0e-23
Match length	172
% identity	90
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106
Seq. No.	400580
Seq. ID	LIB3431-035-P1-N1-C8
Method	BLASTN
NCBI GI	g5042437
BLAST score	325
E value	0.0e+00
Match length	389
% identity	100

NCBI Description	Oryza sativa BAC T49B20 genomic sequence, complete sequence
Seq. No.	400581
Seq. ID	LIB3431-035-P1-N1-C9
Method	BLASTX
NCBI GI	g347451
BLAST score	237
E value	7.0e-20
Match length	47
% identity	98
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]
Seq. No.	400582
Seq. ID	LIB3431-035-P1-N1-D1
Method	BLASTX
NCBI GI	g1173347
BLAST score	190
E value	2.0e-14
Match length	41
% identity	95
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_(X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]
Seq. No.	400583
Seq. ID	LIB3431-035-P1-N1-D10
Method	BLASTX
NCBI GI	g82080
BLAST score	256
E value	3.0e-25
Match length	76
% identity	82
NCBI Description	chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf_1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]
Seq. No.	400584
Seq. ID	LIB3431-035-P1-N1-D11
Method	BLASTX
NCBI GI	g170131
BLAST score	152
E value	6.0e-10
Match length	47
% identity	66
NCBI Description	(M55322) ribosomal protein 30S subunit [Spinacia oleracea]
Seq. No.	400585
Seq. ID	LIB3431-035-P1-N1-D12
Method	BLASTN
NCBI GI	g2773153
BLAST score	364
E value	0.0e+00
Match length	388

Match length	94
% identity	91
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE III CAB-13) >gi_72748_pir_CDT033 chlorophyll a/b-binding protein type III precursor (cab-13) - tomato >gi_19277_emb_CAA42818_ (X60275) LHCII type III [Lycopersicon esculentum]
Seq. No.	400596
Seq. ID	LIB3431-035-P1-N1-E6
Method	BLASTX
NCBI GI	g115768
BLAST score	223
E value	4.0e-18
Match length	43
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi_72743_pir_CDKV chlorophyll a/b-binding protein precursor - cucumber (fragment) >gi_167523 (M16057) chlorophyll a/b-binding protein [Cucumis sativus]
Seq. No.	400597
Seq. ID	LIB3431-035-P1-N1-E9
Method	BLASTX
NCBI GI	g2582822
BLAST score	362
E value	2.0e-34
Match length	79
% identity	85
NCBI Description	(Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]
Seq. No.	400598
Seq. ID	LIB3431-035-P1-N1-F1
Method	BLASTX
NCBI GI	g671737
BLAST score	199
E value	2.0e-15
Match length	37
% identity	100
NCBI Description	(X74731) Chlorophyll a/b binding protein [Amaranthus hypochondriacus]
Seq. No.	400599
Seq. ID	LIB3431-035-P1-N1-F10
Method	BLASTX
NCBI GI	g115813
BLAST score	230
E value	6.0e-19
Match length	55
% identity	82
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.	400600
Seq. ID	LIB3431-035-P1-N1-F7

09584015-101000

Match length	69
% identity	100
NCBI Description	(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]
Seq. No.	400611
Seq. ID	LIB3431-035-P1-N1-H11
Method	BLASTN
NCBI GI	g3377792
BLAST score	263
E value	1.0e-146
Match length	334
% identity	95
NCBI Description	Oryza sativa ribulose-1,5-bisphosphate carboxylase/oxygenase activase (rca) mRNA, complete cds
Seq. No.	400612
Seq. ID	LIB3431-035-P1-N1-H12
Method	BLASTN
NCBI GI	g6063530
BLAST score	364
E value	0.0e+00
Match length	389
% identity	98
NCBI Description	Oryza sativa genomic DNA, chromosome 3, clone:P0043E01
Seq. No.	400613
Seq. ID	LIB3431-035-P1-N1-H2
Method	BLASTX
NCBI GI	g1172813
BLAST score	450
E value	1.0e-44
Match length	88
% identity	98
NCBI Description	60S RIBOSOMAL PROTEIN L10-2 (PUTATIVE TUMOR SUPPRESSOR SG12) >gi_1076752_pir_S49596 ribosomal protein L10.e, cytosolic - rice >gi_575357_emb_CAA57340_ (X81692) putative tumor supressor [Oryza sativa]
Seq. No.	400614
Seq. ID	LIB3431-035-P1-N1-H4
Method	BLASTX
NCBI GI	g417260
BLAST score	300
E value	3.0e-27
Match length	81
% identity	70
NCBI Description	LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]
Seq. No.	400615
Seq. ID	LIB3431-035-P1-N1-H5
Method	BLASTX
NCBI GI	g115813
BLAST score	171
E value	4.0e-12

Method	BLASTN
NCBI GI	g19094
BLAST score	52
E value	4.0e-20
Match length	64
% identity	95
NCBI Description	H.vulgare mRNA PsaN for photosystem I subunit N
Seq. No.	400626
Seq. ID	LIB3431-036-P1-K1-B3
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	9.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]
Seq. No.	400627
Seq. ID	LIB3431-036-P1-K1-B4
Method	BLASTX
NCBI GI	g2306981
BLAST score	385
E value	4.0e-37
Match length	68
% identity	99
NCBI Description	(AF010321) photosystem I antenna protein [Oryza sativa]
Seq. No.	400628
Seq. ID	LIB3431-036-P1-K1-B5
Method	BLASTX
NCBI GI	g132105
BLAST score	567
E value	2.0e-58
Match length	122
% identity	87
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538 (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]
Seq. No.	400629
Seq. ID	LIB3431-036-P1-K1-B6
Method	BLASTX
NCBI GI	g4760553
BLAST score	703
E value	2.0e-74
Match length	142
% identity	96
NCBI Description	(AB019533) Nad-dependent formate dehydrogenase [Oryza

0964016-101000

```
Seq. No.          400631
Seq. ID           LIB3431-036-P1-K1-B9
Method            BLASTX
NCBI GI           g320618
BLAST score       486
E value           5.0e-49
Match length      111
% identity        84
NCBI Description  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
```

```
Seq. No.          400632
Seq. ID           LIB3431-036-P1-K1-C1
Method            BLASTX
NCBI GI           g1835731
BLAST score       378
E value           3.0e-36
Match length      122
% identity        67
NCBI Description   (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
```

```
Seq. No.      400633
Seq. ID      LIB3431-036-P1-K1-C11
Method       BLASTX
NCBI GI      g3126854
BLAST score   715
E value      7.0e-76
Match length  136
% identity    99
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```

```
Seq. No.      400634
Seq. ID      LIB3431-036-P1-K1-C12
Method       BLASTX
NCBI GI      g82080
BLAST score   425
E value      7.0e-42
Match length  121
% identity    68
NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
                  >gi_226872_prf_1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
```


Seq. No.	400645
Seq. ID	LIB3431-036-P1-K1-D5
Method	BLASTX
NCBI GI	g4519936
BLAST score	481
E value	2.0e-48
Match length	136
% identity	71
NCBI Description	(AB019186) RPR1 [Oryza sativa]

```
Seq. No.      400647
Seq. ID      LIB3431-036-P1-K1-D7
Method       BLASTX
NCBI GI      g3789954
BLAST score   582
E value      3.0e-60
Match length  109
% identity    100
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza
sativa]
```

```
Seq. No.      400649
Seq. ID      LIB3431-036-P1-K1-E1
Method       BLASTX
```


BLAST score 237
 E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 400660
 Seq. ID LIB3431-036-P1-K1-F12
 Method BLASTN
 NCBI GI g1245938
 BLAST score 36
 E value 1.0e-10
 Match length 36
 % identity 100
 NCBI Description rabClC-2 beta=chloride channel ClC-2G isoform [rabbits,
 heart atrium, mRNA, 2998 nt]

Seq. No. 400661
 Seq. ID LIB3431-036-P1-K1-F2
 Method BLASTX
 NCBI GI g6017100
 BLAST score 588
 E value 6.0e-61
 Match length 142
 % identity 71
 NCBI Description (AC009895) unknown protein [Arabidopsis thaliana]

Seq. No. 400662
 Seq. ID LIB3431-036-P1-K1-F3
 Method BLASTX
 NCBI GI g131388
 BLAST score 383
 E value 6.0e-37
 Match length 127
 % identity 66
 NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
 SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
 THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir_S16260
 photosystem II oxygen-evolving complex protein 1 - common
 wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408)
 33kDa oxygen evolving protein of photosystem II [Triticum
 aestivum]

Seq. No. 400663
 Seq. ID LIB3431-036-P1-K1-F4
 Method BLASTX
 NCBI GI g3789952
 BLAST score 275
 E value 3.0e-24
 Match length 55
 % identity 96
 NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza
 sativa]

Seq. No. 400664

Seq. ID LIB3431-036-P1-K1-F6
 Method BLASTX
 NCBI GI g4558549
 BLAST score 627
 E value 2.0e-65
 Match length 144
 % identity 83
 NCBI Description (AC007138) putative SecA-type chloroplast protein transport factor [*Arabidopsis thaliana*]

Seq. No. 400665
 Seq. ID LIB3431-036-P1-K1-F7
 Method BLASTX
 NCBI GI g2191152
 BLAST score 149
 E value 2.0e-09
 Match length 105
 % identity 39
 NCBI Description (AF007269) A_IG002N01.31 gene product [*Arabidopsis thaliana*]

Seq. No. 400666
 Seq. ID LIB3431-036-P1-K1-F8
 Method BLASTX
 NCBI GI g2407281
 BLAST score 682
 E value 6.0e-72
 Match length 127
 % identity 99
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [*Oryza sativa*]

Seq. No. 400667
 Seq. ID LIB3431-036-P1-K1-G1
 Method BLASTX
 NCBI GI g2130052
 BLAST score 451
 E value 7.0e-45
 Match length 99
 % identity 89
 NCBI Description xylose isomerase (EC 5.3.1.5) - barley
 >gi_1296809_emb_CAA64545_ (X95257) xylose isomerase [*Hordeum vulgare*]

Seq. No. 400668
 Seq. ID LIB3431-036-P1-K1-G10
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [*Oryza sativa*]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [*Oryza sativa*]

Seq. No. 400669

Seq. ID	LIB3431-036-P1-K1-G2
Method	BLASTX
NCBI GI	g3913808
BLAST score	590
E value	4.0e-61
Match length	132
% identity	89
NCBI Description	FERROCHELATASE PRECURSOR (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) >gi_2429618_dbj_BAA22284_ (AB007120) ferrochelatase [Oryza sativa]
Seq. No.	400670
Seq. ID	LIB3431-036-P1-K1-G4
Method	BLASTX
NCBI GI	g4079798
BLAST score	496
E value	4.0e-50
Match length	127
% identity	77
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]
Seq. No.	400671
Seq. ID	LIB3431-036-P1-K1-G5
Method	BLASTX
NCBI GI	g3126854
BLAST score	511
E value	6.0e-52
Match length	99
% identity	97
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.	400672
Seq. ID	LIB3431-036-P1-K1-G6
Method	BLASTX
NCBI GI	g4895205
BLAST score	248
E value	4.0e-21
Match length	61
% identity	77
NCBI Description	(AC007661) putative alcohol dehydrogenase [Arabidopsis thaliana]
Seq. No.	400673
Seq. ID	LIB3431-036-P1-K1-G7
Method	BLASTX
NCBI GI	g2695931
BLAST score	350
E value	5.0e-33
Match length	141
% identity	53
NCBI Description	(AJ222779) hypothetical protein [Hordeum vulgare]
Seq. No.	400674
Seq. ID	LIB3431-036-P1-K1-G8
Method	BLASTN
NCBI GI	g6015437

[Hordeum vulgare]

Seq. No. 400679
Seq. ID LIB3431-036-P1-K1-H9
Method BLASTX
NCBI GI g1709846
BLAST score 164
E value 3.0e-11
Match length 121
% identity 44
NCBI Description PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_706853 (U04336)
22 kDa component of photosystem II [Lycopersicon
esculentum]

Seq. No. 400680
Seq. ID LIB3431-036-P1-N1-A1
Method BLASTN
NCBI GI g576770
BLAST score 280
E value 1.0e-156
Match length 304
% identity 98
NCBI Description Oryza sativa clone ST1 sucrose-regulated mRNA, 3'-end
sequence

Seq. No. 400681
Seq. ID LIB3431-036-P1-N1-A11
Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 1.0e-19
Match length 44
% identity 100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
protein [Oryza sativa]

Seq. No. 400682
Seq. ID LIB3431-036-P1-N1-A4
Method BLASTX
NCBI GI g6103011
BLAST score 515
E value 2.0e-52
Match length 115
% identity 48
NCBI Description (X84225) precursor of photosystem II subunit (22KDa)
[Nicotiana tabacum]

Seq. No. 400683
Seq. ID LIB3431-036-P1-N1-A5
Method BLASTN
NCBI GI g6016845
BLAST score 206
E value 1.0e-112
Match length 347
% identity 89
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

E value 1.0e-19
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 400689
 Seq. ID LIB3431-036-P1-N1-B4
 Method BLASTX
 NCBI GI g2306981
 BLAST score 236
 E value 1.0e-19
 Match length 52
 % identity 87
 NCBI Description (AF010321) photosystem I antenna protein [Oryza sativa]

Seq. No. 400690
 Seq. ID LIB3431-036-P1-N1-B5
 Method BLASTX
 NCBI GI g132105
 BLAST score 443
 E value 7.0e-44
 Match length 80
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 400691
 Seq. ID LIB3431-036-P1-N1-B6
 Method BLASTX
 NCBI GI g4760553
 BLAST score 429
 E value 3.0e-42
 Match length 82
 % identity 95
 NCBI Description (AB019533) Nad-dependent formate dehydrogenase [Oryza
 sativa]

Seq. No. 400692
 Seq. ID LIB3431-036-P1-N1-B7
 Method BLASTX
 NCBI GI g115794
 BLAST score 550
 E value 2.0e-56
 Match length 111
 % identity 94
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
 III CAB-13) >gi_72748_pir_CDT033 chlorophyll a/b-binding
 protein type III precursor (cab-13) - tomato


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% identity          92
NCBI Description    3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURSOR
                    (BETA-KETOACYL-ACP SYNTHASE I) (KAS I)
                    >gi_100555_pir_A39356 3-oxoacyl-[acyl-carrier-protein]
                    synthase (EC 2.3.1.41) I beta chain precursor, chloroplast
                    - barley >gi_167065 (M60410) beta-ketoacyl-ACP synthase I
                    [Hordeum vulgare]

Seq. No.            400698
Seq. ID              LIB3431-036-P1-N1-C9
Method              BLASTX
NCBI GI              g2511594
BLAST score          326
E value              4.0e-30
Match length         95
% identity           66
NCBI Description     (Y13694) multicatalytic endopeptidase complex, proteasome
                    precursor, beta subunit [Arabidopsis thaliana]
                    >gi_2827525_emb_CAA16533.1 (AL021633) multicatalytic
                    endopeptidase complex, proteasome precursor, beta subunit
                    [Arabidopsis thaliana] >gi_3421099 (AF043529) 20S
                    proteasome subunit PBA1 [Arabidopsis thaliana]

Seq. No.            400699
Seq. ID              LIB3431-036-P1-N1-D1
Method              BLASTX
NCBI GI              g4105561
BLAST score          391
E value              9.0e-38
Match length         85
% identity           88
NCBI Description     (AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]

Seq. No.            400700
Seq. ID              LIB3431-036-P1-N1-D10
Method              BLASTX
NCBI GI              g3036942
BLAST score          363
E value              2.0e-34
Match length         71
% identity           97
NCBI Description     (AB012636) light harvesting chlorophyll a/b-binding protein
                    [Nicotiana sylvestris]

Seq. No.            400701
Seq. ID              LIB3431-036-P1-N1-D11
Method              BLASTX
NCBI GI              g482311
BLAST score          428
E value              4.0e-42
Match length         86
% identity           99
NCBI Description     photosystem II oxygen-evolving complex protein 1 - rice
                    (strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving
                    complex protein 1 [Oryza sativa]

Seq. No.            400702

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09584016-101000

% identity 66
NCBI Description (X97606) abscisic acid activated [Medicago sativa]

Seq. No. 400723
Seq. ID LIB3431-036-P1-N1-G7
Method BLASTX
NCBI GI g2695931
BLAST score 504
E value 5.0e-51
Match length 106
% identity 89
NCBI Description (AJ222779) hypothetical protein [Hordeum vulgare]

Seq. No. 400724
Seq. ID LIB3431-036-P1-N1-G9
Method BLASTX
NCBI GI g6063542
BLAST score 390
E value 1.0e-37
Match length 71
% identity 100
NCBI Description (AP000615) EST C74302(E30840) corresponds to a region of the predicted gene.; similar to glyceraldehyde-3-phosphate dehydrogenase. (M64118) [Oryza sativa]

Seq. No. 400725
Seq. ID LIB3431-036-P1-N1-H11
Method BLASTX
NCBI GI g115774
BLAST score 189
E value 4.0e-14
Match length 65
% identity 57
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE I CAB-13) (LHCP) >gi_72731_pir_CDPJ13 chlorophyll a/b-binding protein 13 precursor - petunia
>gi_20471_emb_CAA26210_(X02357) cab 13 precursor polypeptide (aa -33 to 233) [Petunia sp.]

Seq. No. 400726
Seq. ID LIB3431-036-P1-N1-H12
Method BLASTX
NCBI GI g552740
BLAST score 197
E value 2.0e-15
Match length 56
% identity 75
NCBI Description (M17841) ribosomal protein S7 [Zea mays]

Seq. No. 400727
Seq. ID LIB3431-036-P1-N1-H2
Method BLASTX
NCBI GI g6016428
BLAST score 301
E value 3.0e-27
Match length 63
% identity 83

0-98476-7000

0-98476-7000

NCBI Description RIBULOSE BISPHTOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 400771
Seq. ID LIB3431-037-P1-K1-E6
Method BLASTX
NCBI GI g132105
BLAST score 286
E value 2.0e-25
Match length 118
% identity 59

NCBI Description RIBULOSE BISPHTOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 400772
Seq. ID LIB3431-037-P1-K1-E7
Method BLASTX
NCBI GI g1076724
BLAST score 410
E value 5.0e-40
Match length 78
% identity 95

NCBI Description LHCI-680, photosystem I antenna protein - barley
>gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
antenna protein [Hordeum vulgare]

Seq. No. 400773
Seq. ID LIB3431-037-P1-K1-E8
Method BLASTX
NCBI GI g461999
BLAST score 708
E value 6.0e-75
Match length 154
% identity 90

NCBI Description ELONGATION FACTOR G, CHLOROPLAST PRECURSOR (EF-G)

Seq. No. 400774
Seq. ID LIB3431-037-P1-K1-E9
Method BLASTX
NCBI GI g118170
BLAST score 429
E value 3.0e-42
Match length 102

Seq. No. 400784
 Seq. ID LIB3431-037-P1-K1-F9
 Method BLASTX
 NCBI GI g417260
 BLAST score 421
 E value 3.0e-41
 Match length 128
 % identity 66
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

Seq. No. 400785
 Seq. ID LIB3431-037-P1-K1-G10
 Method BLASTX
 NCBI GI g2347098
 BLAST score 448
 E value 2.0e-44
 Match length 94
 % identity 86
 NCBI Description (U76845) ubiquitin-specific protease [Arabidopsis thaliana]
 >gi_4490742_emb_CAB38904.1_ (AL035708) ubiquitin-specific
 protease (AtUBP3) [Arabidopsis thaliana]

Seq. No. 400786
 Seq. ID LIB3431-037-P1-K1-G12
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 1.0e-19
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 400787
 Seq. ID LIB3431-037-P1-K1-G2
 Method BLASTX
 NCBI GI g2501189
 BLAST score 520
 E value 6.0e-53
 Match length 138
 % identity 76
 NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
 >gi_2130146_pir_S61419 thiamine biosynthetic enzyme thil-1
 - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
 [Zea mays]

Seq. No. 400788
 Seq. ID LIB3431-037-P1-K1-G3
 Method BLASTX
 NCBI GI g2565436
 BLAST score 159
 E value 1.0e-10
 Match length 99

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Seq. No.      400809
Seq. ID      LIB3431-037-P1-N1-B3
Method       BLASTN
NCBI GI      g3885891
BLAST score   262
E value      1.0e-145
Match length  330
% identity    95
NCBI Description  Oryza sativa photosystem-1 F subunit precursor (PSI-F)
                mRNA, complete cds
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Seq. No.      400811
Seq. ID       LIB3431-037-P1-N1-C10
Method        BLASTX
NCBI GI       g2191138
BLAST score    253
E value       1.0e-21
Match length   73
% identity     70
NCBI Description (AF007269) A_IG002N01.18 gene product [Arabidopsis thaliana]
```

51358

Match length	41
% identity	66
NCBI Description	(AC006193) Putative membrane related protein [Arabidopsis thaliana]
Seq. No.	400813
Seq. ID	LIB3431-037-P1-N1-C6
Method	BLASTX
NCBI GI	g3885892
BLAST score	471
E value	4.0e-47
Match length	89
% identity	100
NCBI Description	(AF093634) photosystem-1 F subunit precursor [Oryza sativa]
Seq. No.	400814
Seq. ID	LIB3431-037-P1-N1-C8
Method	BLASTX
NCBI GI	g3345477
BLAST score	182
E value	2.0e-13
Match length	34
% identity	97
NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.	400815
Seq. ID	LIB3431-037-P1-N1-C9
Method	BLASTX
NCBI GI	g3885886
BLAST score	199
E value	3.0e-15
Match length	35
% identity	100
NCBI Description	(AF093631) Rieske Fe-S precursor protein [Oryza sativa]
Seq. No.	400816
Seq. ID	LIB3431-037-P1-N1-D1
Method	BLASTX
NCBI GI	g3789952
BLAST score	203
E value	1.0e-15
Match length	37
% identity	100
NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]
Seq. No.	400817
Seq. ID	LIB3431-037-P1-N1-D10
Method	BLASTX
NCBI GI	g671740
BLAST score	263
E value	9.0e-23
Match length	51
% identity	100
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]

mays]

Seq. No. 400833
 Seq. ID LIB3431-037-P1-N1-F4
 Method BLASTX
 NCBI GI g128690
 BLAST score 533
 E value 2.0e-54
 Match length 120
 % identity 88
 NCBI Description NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 3, CHLOROPLAST
 >gi_66161_pir_DERZN3 NADH dehydrogenase (ubiquinone) (EC
 1.6.5.3) chain 3 - rice chloroplast >gi_11989_emb_CAA34001_
 (X15901) ndhC; NADH dehydrogenase ND3 [Oryza sativa]
 >gi_226610_prf_1603356AG NADH dehydrogenase ND3 [Oryza
 sativa]

Seq. No. 400834
 Seq. ID LIB3431-037-P1-N1-F5
 Method BLASTX
 NCBI GI g131176
 BLAST score 333
 E value 6.0e-31
 Match length 65
 % identity 97
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR
 (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
 >gi_72683_pir_F1BH4 photosystem I chain IV precursor -
 barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA
 -46 to 101) [Hordeum vulgare] >gi_226163_prf_1413233A
 10.8kD photosystem I protein [Hordeum vulgare var.
 distichum]

Seq. No. 400835
 Seq. ID LIB3431-037-P1-N1-F6
 Method BLASTX
 NCBI GI g548605
 BLAST score 277
 E value 2.0e-24
 Match length 59
 % identity 90
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
 (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
 >gi_539055_pir_A48527 photosystem I protein psaK precursor
 - barley >gi_304220 (L12707) photosystem I PSI-K subunit
 [Hordeum vulgare]

Seq. No. 400836
 Seq. ID LIB3431-037-P1-N1-F8
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 1.0e-19
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

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protein 2R precursor - rice >gi_20182_emb_CAA32109
(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
[Oryza sativa]

Seq. No. 400847
Seq. ID LIB3431-037-P1-N1-H1
Method BLASTX
NCBI GI g3294467
BLAST score 369
E value 3.0e-35
Match length 78
% identity 95
NCBI Description (U89341) phosphoglucomutase 1 [Zea mays]

Seq. No. 400848
Seq. ID LIB3431-037-P1-N1-H10
Method BLASTX
NCBI GI g517500
BLAST score 190
E value 5.0e-23
Match length 94
% identity 68
NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa
protein [Zea mays] >gi_444338_prf_1906386A photosystem II
OE17 protein [Pisum sativum]

Seq. No. 400849
Seq. ID LIB3431-037-P1-N1-H11
Method BLASTX
NCBI GI g3126854
BLAST score 415
E value 1.0e-40
Match length 79
% identity 99
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 400850
Seq. ID LIB3431-037-P1-N1-H12
Method BLASTX
NCBI GI g733454
BLAST score 402
E value 3.0e-39
Match length 81
% identity 95
NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
[Zea mays]

Seq. No. 400851
Seq. ID LIB3431-037-P1-N1-H3
Method BLASTX
NCBI GI g482311
BLAST score 374
E value 8.0e-36
Match length 74
% identity 100
NCBI Description photosystem II oxygen-evolving complex protein 1 - rice
(strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving

complex protein 1 [Oryza sativa]

Seq. No. 400852
 Seq. ID LIB3431-037-P1-N1-H4
 Method BLASTX
 NCBI GI g1708924
 BLAST score 252
 E value 2.0e-21
 Match length 54
 % identity 87
 NCBI Description MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NADP-DEPENDENT
 MALIC ENZYME) (NADP-ME) >gi_515759 (L34836) malate
 dehydrogenase (NADP+) [Vitis vinifera]

Seq. No. 400853
 Seq. ID LIB3431-037-P1-N1-H5
 Method BLASTX
 NCBI GI g671740
 BLAST score 202
 E value 1.0e-15
 Match length 38
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
 construct]

Seq. No. 400854
 Seq. ID LIB3431-037-P1-N1-H6
 Method BLASTX
 NCBI GI g4206195
 BLAST score 213
 E value 5.0e-17
 Match length 54
 % identity 67
 NCBI Description (AF071527) hypothetical protein [Arabidopsis thaliana]
 >gi_4262169_gb_AAD14469_ (AC005275) hypothetical protein
 [Arabidopsis thaliana]

Seq. No. 400855
 Seq. ID LIB3431-037-P1-N1-H7
 Method BLASTX
 NCBI GI g548605
 BLAST score 493
 E value 8.0e-50
 Match length 109
 % identity 90
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
 (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
 >gi_539055_pir_A48527 photosystem I protein psaK precursor
 - barley >gi_304220 (L12707) photosystem I PSI-K subunit
 [Hordeum vulgare]

Seq. No. 400856
 Seq. ID LIB3431-037-P1-N1-H8
 Method BLASTX
 NCBI GI g3757515
 BLAST score 305
 E value 8.0e-28

Match length 73
 % identity 77
 NCBI Description (AC005167) hypothetical protein [Arabidopsis thaliana]
 >gi_4581130_gb_AAD24620.1_AC005825_27 (AC005825)
 hypothetical protein [Arabidopsis thaliana]

Seq. No. 400857
 Seq. ID LIB3431-037-P1-N1-H9
 Method BLASTX
 NCBI GI g671740
 BLAST score 264
 E value 5.0e-23
 Match length 53
 % identity 96
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 400858
 Seq. ID LIB3431-038-P1-K1-A1
 Method BLASTX
 NCBI GI g166410
 BLAST score 443
 E value 6.0e-44
 Match length 118
 % identity 71
 NCBI Description (L07291) Alfin-1 [Medicago sativa]

Seq. No. 400859
 Seq. ID LIB3431-038-P1-K1-A10
 Method BLASTX
 NCBI GI g3075488
 BLAST score 634
 E value 2.0e-66
 Match length 117
 % identity 100
 NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 400860
 Seq. ID LIB3431-038-P1-K1-A11
 Method BLASTX
 NCBI GI g3367596
 BLAST score 394
 E value 3.0e-38
 Match length 121
 % identity 59
 NCBI Description (AL031135) putative protein [Arabidopsis thaliana]

Seq. No. 400861
 Seq. ID LIB3431-038-P1-K1-A12
 Method BLASTX
 NCBI GI g729535
 BLAST score 223
 E value 4.0e-18
 Match length 76
 % identity 58
 NCBI Description FERREDOXIN-THIOREDOXIN REDUCTASE, CATALYTIC CHAIN PRECURSOR (FTR-C) (FERREDOXIN-THIOREDOXIN REDUCTASE SUBUNIT B)

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Seq. No.	400863
Seq. ID	LIB3431-038-P1-K1-A3
Method	BLASTX
NCBI GI	g3548808
BLAST score	322
E value	8.0e-30
Match length	81
% identity	67
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

```
Seq. No.      400864
Seq. ID      LIB3431-038-P1-K1-A4
Method       BLASTX
NCBI GI      g5031281
BLAST score   274
E value      4.0e-24
Match length  71
% identity    75
NCBI Description (AF139499) unknown [Prunus armeniaca]
```

Seq. No.	400865
Seq. ID	LIB3431-038-P1-K1-A5
Method	BLASTX
NCBI GI	g2293480
BLAST score	431
E value	2.0e-42
Match length	85
% identity	98
NCBI Description	(AF011331) glycine-rich protein [Oryza sativa]

```
Seq. No.          400866
Seq. ID           LIB3431-038-P1-K1-A7
Method            BLASTX
NCBI GI           g282882
BLAST score       175
E value           2.0e-12
Match length      105
% identity        37
NCBI Description   receptor-like protein kinase precursor - Arabidopsis
                   thaliana >gi_166848 (M84659) receptor-like protein kinase
                   [Arabidopsis thaliana]
```

51369

Method BLASTX
 NCBI GI g3822223
 BLAST score 444
 E value 4.0e-44
 Match length 123
 % identity 61
 NCBI Description (AF077955) branched-chain alpha keto-acid dehydrogenase E1
 alpha subunit [Arabidopsis thaliana]

Seq. No. 400868
 Seq. ID LIB3431-038-P1-K1-B1
 Method BLASTX
 NCBI GI g2293480
 BLAST score 431
 E value 1.0e-42
 Match length 85
 % identity 98
 NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

Seq. No. 400869
 Seq. ID LIB3431-038-P1-K1-B10
 Method BLASTX
 NCBI GI g4689384
 BLAST score 231
 E value 4.0e-19
 Match length 43
 % identity 100
 NCBI Description (AF139467) LHCII type I chlorophyll a/b binding protein
 [Vigna radiata]

Seq. No. 400870
 Seq. ID LIB3431-038-P1-K1-B11
 Method BLASTX
 NCBI GI g5734748
 BLAST score 206
 E value 4.0e-16
 Match length 129
 % identity 36
 NCBI Description (AC007651) Unknown protein [Arabidopsis thaliana]

Seq. No. 400871
 Seq. ID LIB3431-038-P1-K1-B3
 Method BLASTN
 NCBI GI g4959460
 BLAST score 35
 E value 5.0e-10
 Match length 35
 % identity 100
 NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No. 400872
 Seq. ID LIB3431-038-P1-K1-B4
 Method BLASTX
 NCBI GI g2501190
 BLAST score 602
 E value 1.0e-62
 Match length 142

% identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 400878
 Seq. ID LIB3431-038-P1-K1-C10
 Method BLASTX
 NCBI GI g167097
 BLAST score 188
 E value 9.0e-27
 Match length 76
 % identity 82
 NCBI Description (M55449) ribulose 1,5-bisphosphate carboxylase activase
 [Hordeum vulgare]

Seq. No. 400879
 Seq. ID LIB3431-038-P1-K1-C11
 Method BLASTX
 NCBI GI g4204263
 BLAST score 349
 E value 6.0e-33
 Match length 113
 % identity 60
 NCBI Description (AC005223) 40409 [Arabidopsis thaliana]

Seq. No. 400880
 Seq. ID LIB3431-038-P1-K1-C12
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 8.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 400881
 Seq. ID LIB3431-038-P1-K1-C2
 Method BLASTX
 NCBI GI g320618
 BLAST score 333
 E value 4.0e-31
 Match length 92
 % identity 74
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

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squarrosa >gi_599620_emb_CAA58150_ (X83095) rbcS gene
[Aegilops squarrosa]

Seq. No. 400892
Seq. ID LIB3431-038-P1-K1-D5
Method BLASTX
NCBI GI g131225
BLAST score 586
E value 1.0e-60
Match length 144
% identity 78
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 400893
Seq. ID LIB3431-038-P1-K1-D7
Method BLASTX
NCBI GI g4582445
BLAST score 269
E value 2.0e-23
Match length 64
% identity 70
NCBI Description (AC007071) unknown protein [Arabidopsis thaliana]
>gi_4589952_gb_AAD26470.1 AC007169_2 (AC007169) unknown protein [Arabidopsis thaliana]

Seq. No. 400894
Seq. ID LIB3431-038-P1-K1-D9
Method BLASTX
NCBI GI g2760334
BLAST score 294
E value 2.0e-26
Match length 76
% identity 64
NCBI Description (AC002130) F1N21.5 [Arabidopsis thaliana]

Seq. No. 400895
Seq. ID LIB3431-038-P1-K1-E1
Method BLASTX
NCBI GI g1001532
BLAST score 251
E value 2.0e-21
Match length 93
% identity 52
NCBI Description (D64000) hypothetical protein [Synechocystis sp.]

Seq. No. 400896
Seq. ID LIB3431-038-P1-K1-E10
Method BLASTX
NCBI GI g82080
BLAST score 638
E value 8.0e-67
Match length 140
% identity 81
NCBI Description chlorophyll a/b-binding protein type III precursor - tomato

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Seq. No.      400905
Seq. ID      LIB3431-038-P1-K1-F11
Method       BLASTX
NCBI GI      g132105
BLAST score   322
E value      4.0e-46
Match length  110
% identity    87
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                (D00643) small subunit of ribulose-1,5-bisphosphate
                carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
```


09684016 101000

```
Seq. No.      400917
Seq. ID      LIB3431-038-P1-K1-G8
Method       BLASTX
NCBI GI      g733454
BLAST score   604
E value      8.0e-63
Match length  138
% identity    83
NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
               [Zea mays]
```

```
Seq. No.      400919
Seq. ID      LIB3431-038-P1-K1-H11
Method       BLASTX
NCBI GI      g1170937
BLAST score   760
E value      4.0e-81
Match length  144
% identity    100
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
synthetase [Oryza sativa]
```

51380

0001015-101000

Seq. ID LIB3431-038-P1-K1-H6
 Method BLASTX
 NCBI GI g132105
 BLAST score 591
 E value 3.0e-61
 Match length 127
 % identity 87
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 400926
 Seq. ID LIB3431-038-P1-K1-H7
 Method BLASTN
 NCBI GI g1245938
 BLAST score 36
 E value 1.0e-10
 Match length 36
 % identity 100
 NCBI Description rabClC-2 beta=chloride channel ClC-2G isoform [rabbits, heart atrium, mRNA, 2998 nt]

Seq. No. 400927
 Seq. ID LIB3431-038-P1-K1-H8
 Method BLASTX
 NCBI GI g5007084
 BLAST score 729
 E value 2.0e-77
 Match length 137
 % identity 100
 NCBI Description (AF155333) NADP-specific isocitrate dehydrogenase [Oryza sativa]

Seq. No. 400928
 Seq. ID LIB3431-038-P1-K1-H9
 Method BLASTX
 NCBI GI g6006363
 BLAST score 267
 E value 3.0e-23
 Match length 50
 % identity 100
 NCBI Description (AP000559) ESTs AU078183(C62904),C73912(E21020) correspond to a region of the predicted gene.; Similar to water stress inducible protein (U74296) [Oryza sativa]

Seq. No. 400929
 Seq. ID LIB3431-038-P1-N1-A10
 Method BLASTX
 NCBI GI g3153151
 BLAST score 162
 E value 5.0e-11

00000000000000000000000000000000

```
Seq. No.      400936
Seq. ID      LIB3431-038-P1-N1-B1
Method       BLASTN
NCBI GI      g2331130
BLAST score   187
E value      1.0e-101
Match length  235
% identity    95
NCBI Description  Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds
```

Seq. No.	400937
Seq. ID	LIB3431-038-P1-N1-B10
Method	BLASTX
NCBI GI	g4689384
BLAST score	231
E value	4.0e-19
Match length	43
% identity	100
NCBI Description	(AF139467) LHCII type I chlorophyll a/b binding protein [Vigna radiata]

```
Seq. No.      400938
Seq. ID       LIB3431-038-P1-N1-B3
Method        BLASTX
NCBI GI       g3192019
BLAST score    146
E value        4.0e-09
Match length   50
% identity     52
NCBI Description (AL023797) uridylyate kinase [Streptomyces coelicolor]
```

```
Seq. No.          400939
Seq. ID           LIB3431-038-P1-N1-B4
Method            BLASTX
NCBI GI           g2501190
BLAST score       155
E value           4.0e-10
Match length      51
% identity        69
NCBI Description   THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
                  >gi_2130147_pir_S61420 thiamine biosynthetic enzyme thil-2
                  - maize >gi_596080 (U17351) thiamine biosynthetic enzyme
                  [Zea mays]
```

```
Seq. No.      400940
Seq. ID      LIB3431-038-P1-N1-B5
Method       BLASTX
NCBI GI      g461595
BLAST score   188
E value      5.0e-14
Match length  98
% identity    44
NCBI Description  ATP SYNTHASE B' CHAIN PRECURSOR (SUBUNIT II)
                >gi_479533_pir_S34473 H+-transporting ATP synthase (EC
                3.6.1.34) chain 9 - spinach >gi_394755_emb_CAA50520_
                (X71397) CF(o)II ATP synthase subunit 9 [Spinacia oleracea]
```

```
Seq. No.      400941
Seq. ID       LIB3431-038-P1-N1-B6
Method        BLASTX
NCBI GI       g710308
BLAST score   338
E value       1.0e-31
Match length  63
% identity    95
NCBI Description (U11693) victorin binding protein [Avena sativa]
```

```
Seq. No.      400942
Seq. ID      LIB3431-038-P1-N1-B8
Method       BLASTX
NCBI GI      g1658271
BLAST score   147
E value      2.0e-09
Match length  40
% identity    78
NCBI Description (U74622) nascent polypeptide associated complex alpha chain
[Nicotiana tabacum]
```

```

Seq. No.      400943
Seq. ID       LIB3431-038-P1-N1-B9
Method        BLASTX
NCBI GI       g132105
BLAST score   354
E value       2.0e-33
Match length  65
% identity    100
NCBI Description  RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphtosphate
                  carboxylase S [Oryza sativa]

```

Seq. No. 400944
Seq. ID LIB3431-038-P1-N1-C1
Method BLASTN
NCBI GI q11957


```
BLAST score      190
E value         3.0e-14
Match length    39
% identity      100
NCBI Description (AF155333) NADP-specific isocitrate dehydrogenase [Oryza
sativa]
```

Seq. No.	400984
Seq. ID	LIB3431-038-P1-N1-H9
Method	BLASTN
NCBI GI	g6006355
BLAST score	198
E value	1.0e-107
Match length	391
% identity	99
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No.	400985
Seq. ID	LIB3431-039-P1-K2-A10
Method	BLASTX
NCBI GI	g3885894
BLAST score	177
E value	3.0e-24
Match length	69
% identity	90
NCBI Description	(AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

```
Seq. No.      400986
Seq. ID      LIB3431-039-P1-K2-A6
Method       BLASTN
NCBI GI      g1835730
BLAST score   75
E value      2.0e-34
Match length  93
% identity   97
NCBI Description  Oryza sativa photosystem II 10 kDa polypeptide mRNA,
                  complete cds
```

```
Seq. No.      400987
Seq. ID       LIB3431-039-P1-K2-A7
Method        BLASTX
NCBI GI       g3808101
BLAST score    532
E value        2.0e-54
Match length   125
% identity     82
NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]
```

Seq. No.	400988
Seq. ID	LIB3431-039-P1-K2-B1
Method	BLASTN
NCBI GI	g606816
BLAST score	53
E value	3.0e-21
Match length	57
% identity	98
NCBI Description	Oryza sativa chloroplast carbonic anhydrase mRNA, complete

SECRET

Seq. No.	400990
Seq. ID	LIB3431-039-P1-K2-B11
Method	BLASTN
NCBI GI	g11957
BLAST score	127
E value	4.0e-65
Match length	251
% identity	88
NCBI Description	Rice complete chloroplast genome

```
Seq. No.      400992
Seq. ID      LIB3431-039-P1-K2-B3
Method       BLASTX
NCBI GI      g733454
BLAST score   483
E value      9.0e-49
Match length  111
% identity    82
NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
               [Zea mays]
```

```
Seq. No.      400993
Seq. ID      LIB3431-039-P1-K2-B6
Method       BLASTX
NCBI GI      g3126854
BLAST score   149
E value      7.0e-10
Match length  30
% identity    100
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```

```
Seq. No.      400994
Seq. ID       LIB3431-039-P1-K2-B7
Method        BLASTX
NCBI GI       g3345477
BLAST score   626
E value       2.0e-65
Match length  120
% identity    99
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
```

```
Seq. No.      400995
Seq. ID       LIB3431-039-P1-K2-B8
Method        BLASTX
NCBI GI       g131166
BLAST score    503
E value       3.0e-51
Match length   97
% identity     96
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
                  (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_82100_pir_S00449
                  photosystem I chain II precursor - tomato >gi_170492
                  (M21344) photosystem I subunit II protein precursor
                  [Lycopersicon esculentum] >gi_226544_prf_1601516A
                  photosystem I reaction center II [Lycopersicon esculentum]
```

```
Seq. No.          400996
Seq. ID           LIB3431-039-P1-K2-C1
Method            BLASTX
NCBI GI           g541950
BLAST score       237
E value           8.0e-20
Match length      69
% identity        67
NCBI Description   SPCP1 protein - soybean >gi_310576 (L12257).nodulin-26
                  [Glycine max]
```

```
Seq. No.      400997
Seq. ID      LIB3431-039-P1-K2-C10
Method       BLASTX
NCBI GI      g289920
BLAST score   238
E value      5.0e-20
Match length  44
% identity    100
NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium
                hirsutum]
```

```
Seq. No.      400998
Seq. ID       LIB3431-039-P1-K2-C3
Method        BLASTX
NCBI GI       g3868758
BLAST score   612
E value       8.0e-64
Match length  114
% identity    96
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
```

Seq. No. 400999
 Seq. ID LIB3431-039-P1-K2-C4
 Method BLASTX
 NCBI GI g1706260
 BLAST score 363
 E value 6.0e-35
 Match length 81
 % identity 85
 NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__S59597
 cysteine proteinase 1 precursor - maize
 >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
 mays]

Seq. No. 401000
 Seq. ID LIB3431-039-P1-K2-C5
 Method BLASTX
 NCBI GI g3126854
 BLAST score 772
 E value 2.0e-82
 Match length 144
 % identity 99
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401001
 Seq. ID LIB3431-039-P1-K2-C6
 Method BLASTX
 NCBI GI g320618
 BLAST score 464
 E value 2.0e-46
 Match length 107
 % identity 82
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 401002
 Seq. ID LIB3431-039-P1-K2-C7
 Method BLASTN
 NCBI GI g6015437
 BLAST score 37
 E value 2.0e-11
 Match length 48
 % identity 66
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 401003
 Seq. ID LIB3431-039-P1-K2-C8
 Method BLASTX
 NCBI GI g733454
 BLAST score 369
 E value 2.0e-35
 Match length 100
 % identity 71
 NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
 [Zea mays]


```

Method                BLASTX
NCBI GI               g5729704
BLAST score           249
E value               3.0e-21
Match length          102
% identity             45
NCBI Description       (AC007927) unknown protein, 5' partial [Arabidopsis
                        thaliana]

Seq. No.              401019
Seq. ID               LIB3431-039-P1-K2-F8
Method                BLASTX
NCBI GI               g1773330
BLAST score           636
E value               2.0e-66
Match length          148
% identity             84
NCBI Description       (U80071) glycolate oxidase [Mesembryanthemum crystallinum]

```

```
Seq. No.          401019
Seq. ID           LIB3431-039-P1-K2-F8
Method            BLASTX
NCBI GI           g1773330
BLAST score       636
E value           2.0e-66
Match length      148
% identity        84
NCBI Description   (U80071) glycolate oxidase [Mesembryanthemum crystallinum]
```

Seq. No.	401020
Seq. ID	LIB3431-039-P1-K2-F9
Method	BLASTN
NCBI GI	g2073379
BLAST score	228
E value	1.0e-125
Match length	243
% identity	98
NCBI Description	Rice CP26 mRNA, partial sequence

```
Seq. No.          401021
Seq. ID           LIB3431-039-P1-K2-G10
Method            BLASTN
NCBI GI           g6015437
BLAST score       35
E value           5.0e-10
Match length      35
% identity        100
NCBI Description   Homo sapiens PEX1 mRNA, complete cds
```

```
Seq. No.      401022
Seq. ID      LIB3431-039-P1-K2-G12
Method       BLASTX
NCBI GI      g82080
BLAST score   417
E value      6.0e-41
Match length  122
% identity    66
NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
                  >gi_226872_prf__1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
```

```
Seq. No.      401023
Seq. ID      LIB3431-039-P1-K2-G2
Method       BLASTX
NCBI GI      g1729971
BLAST score   238
E value      4.0e-20
```


BLAST score 287
E value 1.0e-25
Match length 56
% identity 96
NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
HYDROLASE) (ADOHCYASE) >gi_169663 (M81885)
S-adenosylhomocysteine hydrolase [Petroselinum crispum]

Seq. No. 401038
Seq. ID LIB3431-039-P1-N1-A6
Method BLASTX
NCBI GI g1835731
BLAST score 403
E value 3.0e-39
Match length 89
% identity 88
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 401039
Seq. ID LIB3431-039-P1-N1-A7
Method BLASTX
NCBI GI g3808101
BLAST score 350
E value 5.0e-33
Match length 80
% identity 90
NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]

Seq. No. 401040
Seq. ID LIB3431-039-P1-N1-A9
Method BLASTX
NCBI GI g1707008
BLAST score 384
E value 4.0e-37
Match length 92
% identity 78
NCBI Description (U78721) 30S ribosomal protein S5 isolog [Arabidopsis
thaliana]

Seq. No. 401041
Seq. ID LIB3431-039-P1-N1-B10
Method BLASTN
NCBI GI g11957
BLAST score 256
E value 1.0e-142
Match length 464
% identity 97
NCBI Description Rice complete chloroplast genome

Seq. No. 401042
Seq. ID LIB3431-039-P1-N1-B2
Method BLASTX
NCBI GI g3036951
BLAST score 333
E value 4.0e-31
Match length 64
% identity 100

Seq. ID LIB3431-039-P1-N1-C5
 Method BLASTX
 NCBI GI g3126854
 BLAST score 299
 E value 5.0e-27
 Match length 58
 % identity 98
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401054
 Seq. ID LIB3431-039-P1-N1-C6
 Method BLASTX
 NCBI GI g3036946
 BLAST score 313
 E value 8.0e-29
 Match length 61
 % identity 98
 NCBI Description (AB012637) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 401055
 Seq. ID LIB3431-039-P1-N1-C8
 Method BLASTN
 NCBI GI g2073379
 BLAST score 71
 E value 1.0e-31
 Match length 139
 % identity 86
 NCBI Description Rice CP26 mRNA, partial sequence

Seq. No. 401056
 Seq. ID LIB3431-039-P1-N1-C9
 Method BLASTN
 NCBI GI g2072554
 BLAST score 277
 E value 1.0e-154
 Match length 341
 % identity 95
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 401057
 Seq. ID LIB3431-039-P1-N1-D3
 Method BLASTN
 NCBI GI g218209
 BLAST score 48
 E value 8.0e-18
 Match length 68
 % identity 93
 NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No. 401058
 Seq. ID LIB3431-039-P1-N1-D4
 Method BLASTX
 NCBI GI g4115416

% identity 93
 NCBI Description (AF139465) LHCII type III chlorophyll a/b binding protein
 [Vigna radiata]

Seq. No. 401064
 Seq. ID LIB3431-039-P1-N1-E7
 Method BLASTX
 NCBI GI g671740
 BLAST score 433
 E value 9.0e-43
 Match length 78
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
 construct]

Seq. No. 401065
 Seq. ID LIB3431-039-P1-N1-F3
 Method BLASTX
 NCBI GI g464980
 BLAST score 415
 E value 1.0e-40
 Match length 80
 % identity 96
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
 LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_166422 (L06967)
 ubiquitin carrier protein [Medicago sativa]

Seq. No. 401066
 Seq. ID LIB3431-039-P1-N1-F6
 Method BLASTX
 NCBI GI g2598589
 BLAST score 234
 E value 2.0e-19
 Match length 70
 % identity 60
 NCBI Description (Y15367) MtN19 [Medicago truncatula]

Seq. No. 401067
 Seq. ID LIB3431-039-P1-N1-F7
 Method BLASTX
 NCBI GI g5729704
 BLAST score 249
 E value 3.0e-21
 Match length 102
 % identity 45
 NCBI Description (AC007927) unknown protein, 5' partial [Arabidopsis
 thaliana]

Seq. No. 401068
 Seq. ID LIB3431-039-P1-N1-F8
 Method BLASTN
 NCBI GI g2570514
 BLAST score 287
 E value 1.0e-160
 Match length 335
 % identity 96
 NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds

Seq. No.	401069
Seq. ID	LIB3431-039-P1-N1-F9
Method	BLASTN
NCBI GI	g2073379
BLAST score	168
E value	2.0e-89
Match length	243
% identity	92
NCBI Description	Rice CP26 mRNA, partial sequence
Seq. No.	401070
Seq. ID	LIB3431-039-P1-N1-G1
Method	BLASTX
NCBI GI	g1168587
BLAST score	200
E value	2.0e-15
Match length	45
% identity	87
NCBI Description	ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR >gi_1084467_pir_S43728 H+-transporting ATP synthase (EC 3.6.1.34) - sorghum >gi_311231_emb_CAA46803_ (X66004) H(+)-transporting ATP synthase [Sorghum bicolor]
Seq. No.	401071
Seq. ID	LIB3431-039-P1-N1-G10
Method	BLASTX
NCBI GI	g1296955
BLAST score	396
E value	2.0e-38
Match length	76
% identity	45
NCBI Description	(X95402) duplicated domain structure protein [Oryza sativa]
Seq. No.	401072
Seq. ID	LIB3431-039-P1-N1-G11
Method	BLASTX
NCBI GI	g1296955
BLAST score	320
E value	2.0e-29
Match length	73
% identity	39
NCBI Description	(X95402) duplicated domain structure protein [Oryza sativa]
Seq. No.	401073
Seq. ID	LIB3431-039-P1-N1-G12
Method	BLASTX
NCBI GI	g115813
BLAST score	257
E value	4.0e-22
Match length	61
% identity	82
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.	401074


```

NCBI GI          g4490317
BLAST score      319
E value         3.0e-29
Match length    158
% identity      42
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No.        401113
Seq. ID         LIB3431-040-P1-K2-E12
Method          BLASTX
NCBI GI         g729668
BLAST score     228
E value         1.0e-18
Match length    66
% identity      61
NCBI Description HISTONE H1 >gi_2147479_pir_S65059 histone H1,
                  drought-inducible - Lycopersicon pennellii >gi_436823
                  (U01890) Solanum pennellii histone H1 [Solanum pennellii]

```

```
Seq. No.          401114
Seq. ID           LIB3431-040-P1-K2-E2
Method            BLASTX
NCBI GI           g120661
BLAST score       198
E value           1.0e-16
Match length      90
% identity        60
NCBI Description   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST
                   PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate
                   dehydrogenase A-subunit precursor [Nicotiana tabacum]
```

```
Seq. No.      201115
Seq. ID      LIB3431-040-P1-K2-E3
Method       BLASTX
NCBI GI      g132105
BLAST score   503
E value      3.0e-51
Match length  104
% identity    88
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                (D00643) small subunit of ribulose-1,5-bisphosphate
                carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                sativa] >gi_226375_prf_1508256A ribulose biphosphate
                carboxylase S [Oryza sativa]
```

Seq. No.	401116
Seq. ID	LIB3431-040-P1-K2-E4
Method	BLASTX
NCBI GI	g2407281
BLAST score	254
E value	3.0e-22
Match length	68
% identity	75

NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 401117
Seq. ID LIB3431-040-P1-K2-E5
Method BLASTN
NCBI GI g3819221
BLAST score 84
E value 3.0e-39
Match length 282
% identity 83
NCBI Description Hordeum vulgare partial mRNA; clone cMWG0721

Seq. No. 401118
Seq. ID LIB3431-040-P1-K2-E8
Method BLASTX
NCBI GI g2407281
BLAST score 455
E value 2.0e-45
Match length 119
% identity 77
NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 401119
Seq. ID LIB3431-040-P1-K2-E9
Method BLASTX
NCBI GI g1174745
BLAST score 359
E value 3.0e-34
Match length 80
% identity 89
NCBI Description TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM)
>gi_1363523_pir_S53761 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - rye
>gi_609262_emb_CAA83533_(Z32521) triosephosphate isomerase [Secale cereale] >gi_1095494_prf_2109226B triosephosphate isomerase [Secale cereale]

Seq. No. 401120
Seq. ID LIB3431-040-P1-K2-F10
Method BLASTX
NCBI GI g3885894
BLAST score 507
E value 2.0e-51
Match length 132
% identity 77
NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No. 401121
Seq. ID LIB3431-040-P1-K2-F11
Method BLASTX
NCBI GI g2104959
BLAST score 324
E value 2.0e-30
Match length 77
% identity 74


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Match length      142
% identity        56
NCBI Description  (AL022604) putative sugar transporter protein [Arabidopsis
                  thaliana]

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Seq. No.	401132
Seq. ID	LIB3431-040-P1-K2-G8
Method	BLASTX
NCBI GI	g3080420
BLAST score	389
E value	1.0e-37
Match length	120
% identity	62
NCBI Description	(AL022604) putative sugar transporter protein [Arabidopsis thaliana]

```
Seq. No.      401133
Seq. ID      LIB3431-040-P1-K2-H10
Method       BLASTN
NCBI GI      g6103440
BLAST score   93
E value      5.0e-45
Match length  149
% identity    91
NCBI Description  Oryza sativa metallothionein-like protein (ML2) mRNA,
complete cds
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Seq. No.	401134
Seq. ID	LIB3431-040-P1-K2-H12
Method	BLASTN
NCBI GI	g2072554
BLAST score	146
E value	3.0e-76
Match length	186
% identity	95
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	401135
Seq. ID	LIB3431-040-P1-K2-H2
Method	BLASTN
NCBI GI	g3135542
BLAST score	39
E value	8.0e-13
Match length	67
% identity	90
NCBI Description	Oryza sativa aquaporin (PIP2a) mRNA, complete cds

Seq. No.	401136
Seq. ID	LIB3431-040-P1-K2-H5
Method	BLASTX
NCBI GI	g4584342
BLAST score	221
E value	6.0e-18
Match length	120
% identity	42
NCBI Description	(AC007127) putative ubiquitin protein [Arabidopsis

thaliana]

Seq. No. 401137
 Seq. ID LIB3431-040-P1-K2-H6
 Method BLASTX
 NCBI GI g4079798
 BLAST score 540
 E value 2.0e-55
 Match length 107
 % identity 99
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 401138
 Seq. ID LIB3431-040-P1-K2-H8
 Method BLASTX
 NCBI GI g2407281
 BLAST score 616
 E value 3.0e-64
 Match length 118
 % identity 97
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 401139
 Seq. ID LIB3431-040-P1-K2-H9
 Method BLASTX
 NCBI GI g2072555
 BLAST score 348
 E value 7.0e-33
 Match length 62
 % identity 98
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 401140
 Seq. ID LIB3431-040-P1-N1-A10
 Method BLASTN
 NCBI GI g2072554
 BLAST score 301
 E value 1.0e-169
 Match length 333
 % identity 98
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 401141
 Seq. ID LIB3431-040-P1-N1-B12
 Method BLASTX
 NCBI GI g2754849
 BLAST score 169
 E value 7.0e-12
 Match length 42
 % identity 79
 NCBI Description (AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

Seq. ID LIB3431-040-P1-N1-F1
 Method BLASTX
 NCBI GI g1174745
 BLAST score 355
 E value 1.0e-33
 Match length 85
 % identity 84
 NCBI Description TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM)
 >gi_1363523_pir_S53761 triose-phosphate isomerase (EC
 5.3.1.1) precursor, chloroplast - rye
 >gi_609262_emb_CAA83533_(Z32521) triosephosphate isomerase
 [Secale cereale] >gi_1095494_prf__2109226B triosephosphate
 isomerase [Secale cereale]

Seq. No. 401161
 Seq. ID LIB3431-040-P1-N1-F11
 Method BLASTX
 NCBI GI g3885894
 BLAST score 233
 E value 2.0e-19
 Match length 61
 % identity 79
 NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No. 401162
 Seq. ID LIB3431-040-P1-N1-F4
 Method BLASTN
 NCBI GI g3345476
 BLAST score 267
 E value 1.0e-148
 Match length 315
 % identity 96
 NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds

Seq. No. 401163
 Seq. ID LIB3431-040-P1-N1-G3
 Method BLASTX
 NCBI GI g167097
 BLAST score 179
 E value 1.0e-25
 Match length 76
 % identity 80
 NCBI Description (M55449) ribulose 1,5-bisphosphate carboxylase activase
 [Hordeum vulgare]

Seq. No. 401164
 Seq. ID LIB3431-040-P1-N1-G4
 Method BLASTX
 NCBI GI g3785996
 BLAST score 238
 E value 5.0e-20
 Match length 97
 % identity 51
 NCBI Description (AC005499) putative annexin [Arabidopsis thaliana]

Seq. No. 401165
 Seq. ID LIB3431-040-P1-N1-G6

Method	BLASTN
NCBI GI	g4138289
BLAST score	354
E value	0.0e+00
Match length	354
% identity	100
NCBI Description	Oryza sativa mRNA for thioredoxin M
Seq. No.	401166
Seq. ID	LIB3431-040-P1-N1-G8
Method	BLASTX
NCBI GI	g3080420
BLAST score	175
E value	2.0e-12
Match length	43
% identity	74
NCBI Description	(AL022604) putative sugar transporter protein [Arabidopsis thaliana]
Seq. No.	401167
Seq. ID	LIB3431-040-P1-N1-H1
Method	BLASTN
NCBI GI	g2072554
BLAST score	370
E value	0.0e+00
Match length	378
% identity	99
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds
Seq. No.	401168
Seq. ID	LIB3431-040-P1-N1-H12
Method	BLASTX
NCBI GI	g4079798
BLAST score	392
E value	6.0e-38
Match length	79
% identity	96
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]
Seq. No.	401169
Seq. ID	LIB3431-040-P1-N1-H3
Method	BLASTX
NCBI GI	g2662310
BLAST score	158
E value	8.0e-21
Match length	56
% identity	90
NCBI Description	(AB009307) bpw1 [Hordeum vulgare]
Seq. No.	401170
Seq. ID	LIB3431-040-P1-N1-H4
Method	BLASTX
NCBI GI	g3126854
BLAST score	343
E value	2.0e-32

BLAST score 277
 E value 2.0e-24
 Match length 52
 % identity 100
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 401176
 Seq. ID LIB3431-041-P1-N1-A4
 Method BLASTX
 NCBI GI g2982301
 BLAST score 255
 E value 8.0e-22
 Match length 91
 % identity 55
 NCBI Description (AF051235) YGL010w-like protein [Picea mariana]

Seq. No. 401177
 Seq. ID LIB3431-041-P1-N1-A6
 Method BLASTX
 NCBI GI g6093827
 BLAST score 169
 E value 1.0e-11
 Match length 97
 % identity 41
 NCBI Description PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME) [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II PROTEIN PSBY-2] >gi_2956690_emb_CAA11248 (AJ223306) PSBY [Arabidopsis thaliana] >gi_3414928 (AF079800) PsbY precursor [Arabidopsis thaliana]

Seq. No. 401178
 Seq. ID LIB3431-041-P1-N1-A7
 Method BLASTX
 NCBI GI g120661
 BLAST score 225
 E value 2.0e-18
 Match length 43
 % identity 95
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate dehydrogenase A-subunit precursor [Nicotiana tabacum]

Seq. No. 401179
 Seq. ID LIB3431-041-P1-N1-A9
 Method BLASTN
 NCBI GI g11640
 BLAST score 45
 E value 4.0e-16
 Match length 137
 % identity 42
 NCBI Description Liverwort Marchantia polymorpha chloroplast genome DNA

Seq. No. 401180
 Seq. ID LIB3431-041-P1-N1-B1
 Method BLASTN
 NCBI GI g2072554

E value 4.0e-24
 Match length 79
 % identity 71
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

Seq. No. 401186
 Seq. ID LIB3431-041-P1-N1-B8
 Method BLASTX
 NCBI GI g2997591
 BLAST score 238
 E value 6.0e-20
 Match length 61
 % identity 79
 NCBI Description (AF020814) glucose-6-phosphate/phosphate-translocator
 precursor [Pisum sativum]

Seq. No. 401187
 Seq. ID LIB3431-041-P1-N1-C1
 Method BLASTX
 NCBI GI g131225
 BLAST score 216
 E value 2.0e-17
 Match length 56
 % identity 73
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
 V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein
 precursor - barley >gi_167087 (M61146) photosystem I
 hydrophobic protein [Hordeum vulgare]

Seq. No. 401188
 Seq. ID LIB3431-041-P1-N1-C10
 Method BLASTX
 NCBI GI g131225
 BLAST score 327
 E value 3.0e-30
 Match length 92
 % identity 70
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
 V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein
 precursor - barley >gi_167087 (M61146) photosystem I
 hydrophobic protein [Hordeum vulgare]

Seq. No. 401189
 Seq. ID LIB3431-041-P1-N1-C11
 Method BLASTN
 NCBI GI g20262
 BLAST score 265
 E value 1.0e-147
 Match length 272
 % identity 99
 NCBI Description O.sativa light-induced mRNA

Seq. No. 401190
 Seq. ID LIB3431-041-P1-N1-C12
 Method BLASTX

NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
complete cds

Seq. No. 401201
Seq. ID LIB3431-041-P1-N1-E8
Method BLASTX
NCBI GI g3386621
BLAST score 157
E value 2.0e-10
Match length 36
% identity 81
NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 401202
Seq. ID LIB3431-041-P1-N1-E9
Method BLASTX
NCBI GI g3980406
BLAST score 360
E value 4.0e-34
Match length 105
% identity 63
NCBI Description (AC004561) putative tropinone reductase [Arabidopsis
thaliana]

Seq. No. 401203
Seq. ID LIB3431-041-P1-N1-F1
Method BLASTX
NCBI GI g3377797
BLAST score 225
E value 2.0e-18
Match length 68
% identity 66
NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for
by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
H36046; coded for by A. thaliana cDNA T44067; coded for by
A. thaliana cDNA T14056; coded for by A. thaliana cDNA
R90691 [Ara]

Seq. No. 401204
Seq. ID LIB3431-041-P1-N1-F12
Method BLASTN
NCBI GI g1835730
BLAST score 123
E value 7.0e-63
Match length 147
% identity 96
NCBI Description Oryza sativa photosystem II 10 kDa polypeptide mRNA,
complete cds

Seq. No. 401205
Seq. ID LIB3431-041-P1-N1-F2
Method BLASTX
NCBI GI g131225
BLAST score 364
E value 1.0e-34
Match length 99
% identity 72

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 401206
Seq. ID LIB3431-041-P1-N1-F3
Method BLASTX
NCBI GI g131225
BLAST score 143
E value 6.0e-09
Match length 53
% identity 49

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 401207
Seq. ID LIB3431-041-P1-N1-F5
Method BLASTN
NCBI GI g2293567
BLAST score 79
E value 2.0e-36
Match length 181
% identity 84
NCBI Description Oryza sativa HvB12D homolog mRNA, complete cds

Seq. No. 401208
Seq. ID LIB3431-041-P1-N1-F7
Method BLASTX
NCBI GI g2980805
BLAST score 322
E value 1.0e-29
Match length 80
% identity 84
NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 401209
Seq. ID LIB3431-041-P1-N1-F9
Method BLASTX
NCBI GI g1084455
BLAST score 362
E value 2.0e-34
Match length 69
% identity 100
NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]

Seq. No. 401210
Seq. ID LIB3431-041-P1-N1-G12
Method BLASTX
NCBI GI g82080
BLAST score 145
E value 1.0e-09
Match length 33
% identity 82

NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
>gi_226872_prf_1609235A chlorophyll a/b binding protein
[Lycopersicon esculentum]

Seq. No. 401211
Seq. ID LIB3431-041-P1-N1-G3
Method BLASTX
NCBI GI g517500
BLAST score 251
E value 1.0e-21
Match length 73
% identity 70

NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa
protein [Zea mays] >gi_444338_prf_1906386A photosystem II
OE17 protein [Pisum sativum]

Seq. No. 401212
Seq. ID LIB3431-041-P1-N1-G4
Method BLASTX
NCBI GI g2696804
BLAST score 152
E value 5.0e-10
Match length 28
% identity 100
NCBI Description (AB009665) water channel protein [Oryza sativa]

Seq. No. 401213
Seq. ID LIB3431-041-P1-N1-H3
Method BLASTX
NCBI GI g347451
BLAST score 351
E value 4.0e-33
Match length 69
% identity 96
NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
sativa]

Seq. No. 401214
Seq. ID LIB3431-041-P1-N1-H6
Method BLASTN
NCBI GI g2570512
BLAST score 48
E value 2.0e-18
Match length 48
% identity 100
NCBI Description Oryza sativa chlorophyll a-b binding protein mRNA, complete
cds

Seq. No. 401215
Seq. ID LIB3431-041-P1-N1-H7
Method BLASTX
NCBI GI g5410350
BLAST score 216
E value 3.0e-17
Match length 45
% identity 91
NCBI Description (AF124045) unknown [Sorghum bicolor]

Seq. No.	401226
Seq. ID	LIB3431-041-P2-K1-B9
Method	BLASTX
NCBI GI	g1652217
BLAST score	269
E value	1.0e-23
Match length	107
% identity	54
NCBI Description	(D90903) hypothetical protein [Synechocystis sp.]
Seq. No.	401227
Seq. ID	LIB3431-041-P2-K1-C11
Method	BLASTX
NCBI GI	g417260
BLAST score	322
E value	1.0e-29
Match length	80
% identity	75
NCBI Description	LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]
Seq. No.	401228
Seq. ID	LIB3431-041-P2-K1-C12
Method	BLASTX
NCBI GI	g4689380
BLAST score	402
E value	2.0e-39
Match length	78
% identity	95
NCBI Description	(AF139465) LHCII type III chlorophyll a/b binding protein [Vigna radiata]
Seq. No.	401229
Seq. ID	LIB3431-041-P2-K1-C2
Method	BLASTX
NCBI GI	g4582455
BLAST score	185
E value	9.0e-14
Match length	99
% identity	36
NCBI Description	(AC007071) putative receptor protein kinase [Arabidopsis thaliana]
Seq. No.	401230
Seq. ID	LIB3431-041-P2-K1-C5
Method	BLASTX
NCBI GI	g2662343
BLAST score	711
E value	2.0e-75
Match length	140
% identity	99
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]
Seq. No.	401231
Seq. ID	LIB3431-041-P2-K1-C7
Method	BLASTX

NCBI GI g3551954
 BLAST score 349
 E value 9.0e-33
 Match length 137
 % identity 51
 NCBI Description (AF082030) senescence-associated protein 5 [Hemerocallis hybrid cultivar]

Seq. No. 401232
 Seq. ID LIB3431-041-P2-K1-C8
 Method BLASTN
 NCBI GI g432606
 BLAST score 75
 E value 4.0e-34
 Match length 154
 % identity 99
 NCBI Description rcl=ras-related GTP binding protein possessing GTPase activity [Oryza sativa=rice, Yamahoushi, callus, mRNA, 955 nt]

Seq. No. 401233
 Seq. ID LIB3431-041-P2-K1-D12
 Method BLASTX
 NCBI GI g1707998
 BLAST score 612
 E value 1.0e-63
 Match length 150
 % identity 80
 NCBI Description SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_481944_pir_S40218 glycine hydroxymethyltransferase (EC 2.1.2.1) - potato >gi_438247_emb_CAA81082_ (Z25863) glycine hydroxymethyltransferase [Solanum tuberosum]

Seq. No. 401234
 Seq. ID LIB3431-041-P2-K1-D2
 Method BLASTN
 NCBI GI g6006355
 BLAST score 132
 E value 6.0e-68
 Match length 197
 % identity 46
 NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No. 401235
 Seq. ID LIB3431-041-P2-K1-D3
 Method BLASTX
 NCBI GI g4877984
 BLAST score 369
 E value 3.0e-35
 Match length 143
 % identity 57
 NCBI Description (AF145755) THA4 [Zea mays]

Seq. No. 401236
 Seq. ID LIB3431-041-P2-K1-D6

Seq. ID LIB3431-041-P2-K1-E2
 Method BLASTN
 NCBI GI g6015437
 BLAST score 36
 E value 3.0e-11
 Match length 36
 % identity 100
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 401242
 Seq. ID LIB3431-041-P2-K1-E3
 Method BLASTX
 NCBI GI g3986695
 BLAST score 519
 E value 7.0e-53
 Match length 122
 % identity 86
 NCBI Description (AF101423) ribosomal protein L12 [Cichorium intybus]

Seq. No. 401243
 Seq. ID LIB3431-041-P2-K1-E5
 Method BLASTX
 NCBI GI g131388
 BLAST score 188
 E value 4.0e-14
 Match length 87
 % identity 56
 NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir_S16260 photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum aestivum]

Seq. No. 401244
 Seq. ID LIB3431-041-P2-K1-E6
 Method BLASTX
 NCBI GI g3075488
 BLAST score 426
 E value 2.0e-51
 Match length 126
 % identity 84
 NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 401245
 Seq. ID LIB3431-041-P2-K1-E7
 Method BLASTN
 NCBI GI g3885887
 BLAST score 355
 E value 0.0e+00
 Match length 363
 % identity 100
 NCBI Description Oryza sativa high mobility group protein (HMG) mRNA, complete cds

Seq. No. 401246

Seq. ID LIB3431-041-P2-K1-E8
 Method BLASTX
 NCBI GI g3386621
 BLAST score 511
 E value 7.0e-52
 Match length 117
 % identity 85
 NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 401247
 Seq. ID LIB3431-041-P2-K1-E9
 Method BLASTX
 NCBI GI g3980400
 BLAST score 487
 E value 5.0e-49
 Match length 166
 % identity 58
 NCBI Description (AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No. 401248
 Seq. ID LIB3431-041-P2-K1-F1
 Method BLASTX
 NCBI GI g3377797
 BLAST score 295
 E value 1.0e-26
 Match length 116
 % identity 53
 NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No. 401249
 Seq. ID LIB3431-041-P2-K1-F11
 Method BLASTN
 NCBI GI g2072554
 BLAST score 307
 E value 1.0e-172
 Match length 319
 % identity 99
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 401250
 Seq. ID LIB3431-041-P2-K1-F12
 Method BLASTX
 NCBI GI g1835731
 BLAST score 537
 E value 7.0e-55
 Match length 114
 % identity 90
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 401251
 Seq. ID LIB3431-041-P2-K1-F2

Method BLASTX
 NCBI GI g131225
 BLAST score 386
 E value 1.0e-37
 Match length 83
 % identity 90
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 401252
 Seq. ID LIB3431-041-P2-K1-F4
 Method BLASTX
 NCBI GI g2660677
 BLAST score 418
 E value 4.0e-41
 Match length 124
 % identity 62
 NCBI Description (AC002342) unknown protein [Arabidopsis thaliana]

Seq. No. 401253
 Seq. ID LIB3431-041-P2-K1-F5
 Method BLASTN
 NCBI GI g2293567
 BLAST score 165
 E value 6.0e-88
 Match length 197
 % identity 96
 NCBI Description Oryza sativa HvB12D homolog mRNA, complete cds

Seq. No. 401254
 Seq. ID LIB3431-041-P2-K1-F6
 Method BLASTN
 NCBI GI g3821780
 BLAST score 36
 E value 8.0e-11
 Match length 36
 % identity 100
 NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 401255
 Seq. ID LIB3431-041-P2-K1-F7
 Method BLASTX
 NCBI GI g2980805
 BLAST score 596
 E value 8.0e-62
 Match length 145
 % identity 77
 NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 401256
 Seq. ID LIB3431-041-P2-K1-F8
 Method BLASTX
 NCBI GI g4007792
 BLAST score 316
 E value 6.0e-29

Seq. No.	401266
Seq. ID	LIB3431-041-P2-K1-H7
Method	BLASTN
NCBI GI	g5410347
BLAST score	90
E value	6.0e-43
Match length	258
% identity	84
NCBI Description	Sorghum bicolor BAC clone 110K5, partial sequence
Seq. No.	401267
Seq. ID	LIB3431-041-P2-K1-H8
Method	BLASTX
NCBI GI	g3126854
BLAST score	634
E value	2.0e-66
Match length	122
% identity	98
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.	401268
Seq. ID	LIB3431-042-P1-K1-A1
Method	BLASTX
NCBI GI	g2407281
BLAST score	662
E value	1.0e-69
Match length	129
% identity	95
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]
Seq. No.	401269
Seq. ID	LIB3431-042-P1-K1-A2
Method	BLASTX
NCBI GI	g4733937
BLAST score	343
E value	3.0e-32
Match length	142
% identity	46
NCBI Description	(AF080245) sesquiterpene synthase [Elaeis oleifera]
Seq. No.	401270
Seq. ID	LIB3431-042-P1-K1-A3
Method	BLASTX
NCBI GI	g3183079
BLAST score	620
E value	1.0e-64
Match length	141
% identity	84
NCBI Description	MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR >gi_1375075_dbj_BAA12870.1_(D85763) glyoxysomal malate dehydrogenase [Oryza sativa]
Seq. No.	401271
Seq. ID	LIB3431-042-P1-K1-A4
Method	BLASTX

NCBI GI g1261917
 BLAST score 318
 E value 3.0e-29
 Match length 98
 % identity 59
 NCBI Description (X96979) lipid transfer protein 7a2b [Hordeum vulgare]

Seq. No. 401272
 Seq. ID LIB3431-042-P1-K1-A5
 Method BLASTX
 NCBI GI g2129608
 BLAST score 594
 E value 1.0e-61
 Match length 138
 % identity 81
 NCBI Description GTP-binding protein, 68K - Arabidopsis thaliana >gi_807577 (L38614) GTP-binding protein [Arabidopsis thaliana]

Seq. No. 401273
 Seq. ID LIB3431-042-P1-K1-A8
 Method BLASTX
 NCBI GI g6056199
 BLAST score 281
 E value 6.0e-25
 Match length 116
 % identity 46
 NCBI Description (AC009400) unknown protein [Arabidopsis thaliana]

Seq. No. 401274
 Seq. ID LIB3431-042-P1-K1-A9
 Method BLASTX
 NCBI GI g347451
 BLAST score 255
 E value 6.0e-22
 Match length 99
 % identity 54
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 401275
 Seq. ID LIB3431-042-P1-K1-B1
 Method BLASTX
 NCBI GI g4972067
 BLAST score 247
 E value 6.0e-21
 Match length 106
 % identity 51
 NCBI Description (AL078467) putative protei [Arabidopsis thaliana]

Seq. No. 401276
 Seq. ID LIB3431-042-P1-K1-B11
 Method BLASTN
 NCBI GI g4959460
 BLAST score 36
 E value 1.0e-10
 Match length 36
 % identity 100

NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No. 401277
Seq. ID LIB3431-042-P1-K1-B12
Method BLASTX
NCBI GI g729135
BLAST score 584
E value 2.0e-60
Match length 144
% identity 76
NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE
(S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID
3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir_S28612
catechol O-methyltransferase (EC 2.1.1.6) - maize
>gi_168532 (M73235) O-methyltransferase [Zea mays]

Seq. No. 401278
Seq. ID LIB3431-042-P1-K1-B3
Method BLASTX
NCBI GI g5733882
BLAST score 299
E value 5.0e-27
Match length 136
% identity 52
NCBI Description (AC007932) Similar to gb_Y12465 serine/threonine kinase
from Sorghum bicolor and contains a PF_00069 Eukaryotic
protein kinase domain. [Arabidopsis thaliana]

Seq. No. 401279
Seq. ID LIB3431-042-P1-K1-B4
Method BLASTX
NCBI GI g2065017
BLAST score 290
E value 5.0e-26
Match length 115
% identity 46
NCBI Description (Y09822) hypothetical protein [Arabidopsis thaliana]

Seq. No. 401280
Seq. ID LIB3431-042-P1-K1-B5
Method BLASTX
NCBI GI g871931
BLAST score 416
E value 9.0e-41
Match length 111
% identity 78
NCBI Description (D30763) ferredoxin [Oryza sativa]

Seq. No. 401281
Seq. ID LIB3431-042-P1-K1-B6
Method BLASTX
NCBI GI g133936
BLAST score 221
E value 6.0e-18
Match length 70
% identity 67
NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi_70867_pir_R3RZ3

E value 3.0e-31
 Match length 111
 % identity 62
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 401291
 Seq. ID LIB3431-042-P1-K1-C9
 Method BLASTX
 NCBI GI g2911068
 BLAST score 199
 E value 2.0e-15
 Match length 43
 % identity 79
 NCBI Description (AL021960) G10-like protein [Arabidopsis thaliana]

Seq. No. 401292
 Seq. ID LIB3431-042-P1-K1-D12
 Method BLASTX
 NCBI GI g322867
 BLAST score 520
 E value 5.0e-53
 Match length 135
 % identity 75
 NCBI Description translation initiation factor eIF-4F isozyme form subunit p82 - wheat

Seq. No. 401293
 Seq. ID LIB3431-042-P1-K1-D3
 Method BLASTX
 NCBI GI g3914603
 BLAST score 287
 E value 1.0e-25
 Match length 134
 % identity 51
 NCBI Description RIBULOSE BISPHTHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]

Seq. No. 401294
 Seq. ID LIB3431-042-P1-K1-D4
 Method BLASTX
 NCBI GI g733454
 BLAST score 503
 E value 6.0e-51
 Match length 118
 % identity 81
 NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No. 401295
 Seq. ID LIB3431-042-P1-K1-D6
 Method BLASTX
 NCBI GI g3913018
 BLAST score 740
 E value 9.0e-79

Seq. No. 401300
 Seq. ID LIB3431-042-P1-K1-E2
 Method BLASTX
 NCBI GI g100796
 BLAST score 712
 E value 2.0e-75
 Match length 143
 % identity 93
 NCBI Description phosphoribulokinase (EC 2.7.1.19) - wheat

Seq. No. 401301
 Seq. ID LIB3431-042-P1-K1-E3
 Method BLASTN
 NCBI GI g902200
 BLAST score 296
 E value 1.0e-166
 Match length 388
 % identity 49
 NCBI Description Z.mays complete chloroplast genome

Seq. No. 401302
 Seq. ID LIB3431-042-P1-K1-E5
 Method BLASTX
 NCBI GI g320618
 BLAST score 472
 E value 2.0e-47
 Match length 105
 % identity 85
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_(D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 401303
 Seq. ID LIB3431-042-P1-K1-E6
 Method BLASTX
 NCBI GI g3582335
 BLAST score 728
 E value 2.0e-77
 Match length 141
 % identity 92
 NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]

Seq. No. 401304
 Seq. ID LIB3431-042-P1-K1-E7
 Method BLASTN
 NCBI GI g2072724
 BLAST score 384
 E value 0.0e+00
 Match length 403
 % identity 99
 NCBI Description O.sativa mRNA for Fd-GOGAT, partial, clone OsGog1

Seq. No. 401305
 Seq. ID LIB3431-042-P1-K1-E8

Method BLASTX
 NCBI GI g132105
 BLAST score 657
 E value 5.0e-69
 Match length 140
 % identity 89
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401306
 Seq. ID LIB3431-042-P1-K1-E9
 Method BLASTX
 NCBI GI g2570515
 BLAST score 640
 E value 5.0e-67
 Match length 134
 % identity 96
 NCBI Description (AF022740) glycolate oxidase [Oryza sativa]

Seq. No. 401307
 Seq. ID LIB3431-042-P1-K1-F1
 Method BLASTX
 NCBI GI g132105
 BLAST score 677
 E value 2.0e-71
 Match length 132
 % identity 95
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401308
 Seq. ID LIB3431-042-P1-K1-F10
 Method BLASTX
 NCBI GI g82080
 BLAST score 432
 E value 1.0e-42
 Match length 122
 % identity 68
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf_1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No. 401309

0964019

Seq. No.	401325
Seq. ID	LIB3431-042-P1-K1-H10
Method	BLASTX
NCBI GI	g3789954
BLAST score	615
E value	4.0e-64
Match length	115
% identity	99
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

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Seq. No.          401327
Seq. ID           LIB3431-042-P1-K1-H2
Method            BLASTX
NCBI GI           g6093778
BLAST score       370
E value           2.0e-35
Match length      103
% identity        75
NCBI Description   PROTEASOME COMPONENT C3 (MACROPAIN SUBUNIT C3)
                   (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C3)
                   >gi_2511574_emb_CAA73619.1_(Y13176) multicatalytic
                   endopeptidase [Arabidopsis thaliana] >gi_3421075 (AF043520)
                   20S proteasome subunit PAB1 [Arabidopsis thaliana]
                   >gi_4966368_gb_AAD34699.1_AC006341.27 (AC006341) Identical
                   to gb_Y13176 Arabidopsis thaliana mRNA for proteasome
                   subunit prc3. ESTs qb H36972, qb T22551 and qb T13800 come

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from this gene

Seq. No. 401328
Seq. ID LIB3431-042-P1-K1-H3
Method BLASTX
NCBI GI g3420052
BLAST score 485
E value 8.0e-51
Match length 137
% identity 77
NCBI Description (AC004680) putative ubiquinone reductase [Arabidopsis thaliana]

Seq. No. 401329
Seq. ID LIB3431-042-P1-K1-H4
Method BLASTX
NCBI GI g3288821
BLAST score 666
E value 4.0e-70
Match length 138
% identity 90
NCBI Description (AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana]
>gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209)
alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

Seq. No. 401330
Seq. ID LIB3431-042-P1-K1-H5
Method BLASTX
NCBI GI g82080
BLAST score 455
E value 2.0e-45
Match length 131
% identity 67
NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
>gi_226872_prf_1609235A chlorophyll a/b binding protein
[Lycopersicon esculentum]

Seq. No. 401331
Seq. ID LIB3431-042-P1-K1-H6
Method BLASTX
NCBI GI g115815
BLAST score 275
E value 1.0e-24
Match length 57
% identity 91
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN M9 PRECURSOR (LHCII TYPE I CAB-M9) (LHCP) >gi_100866_pir_S13098 chlorophyll a/b-binding protein precursor - maize
>gi_22355_emb_CAA39376_(X55892) light-harvesting chlorophyll a/b binding protein [Zea mays]

Seq. No. 401332
Seq. ID LIB3431-042-P1-K1-H7
Method BLASTX
NCBI GI g3914466
BLAST score 366

E value 5.0e-35
 Match length 67
 % identity 97
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
 (PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN
 subunit precursor [Zea mays]

Seq. No. 401333
 Seq. ID LIB3431-042-P1-K1-H9
 Method BLASTN
 NCBI GI g3885887
 BLAST score 371
 E value 0.0e+00
 Match length 378
 % identity 100
 NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
 complete cds

Seq. No. 401334
 Seq. ID LIB3431-042-P1-N1-A3
 Method BLASTX
 NCBI GI g3183079
 BLAST score 210
 E value 1.0e-16
 Match length 58
 % identity 74
 NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
 >gi_1375075_dbj_BAA12870.1 (D85763) glyoxysomal malate
 dehydrogenase [Oryza sativa]

Seq. No. 401335
 Seq. ID LIB3431-042-P1-N1-A4
 Method BLASTX
 NCBI GI g1071925
 BLAST score 194
 E value 9.0e-15
 Match length 51
 % identity 65
 NCBI Description Cw-19 peptide, non specific lipid transfer protein,
 precursor - barley >gi_510528_emb_CAA48623 (X68656) Cw-19
 peptide, non specific lipid transfer protein [Hordeum
 vulgare]

Seq. No. 401336
 Seq. ID LIB3431-042-P1-N1-A5
 Method BLASTX
 NCBI GI g2129825
 BLAST score 391
 E value 1.0e-37
 Match length 93
 % identity 83
 NCBI Description dynamin-like protein phragmoplastin 12 - soybean
 >gi_1217994 (U25547) SDL [Glycine max]

Seq. No. 401337
 Seq. ID LIB3431-042-P1-N1-A8
 Method BLASTX

NCBI GI g6056199
 BLAST score 149
 E value 2.0e-09
 Match length 80
 % identity 39
 NCBI Description (AC009400) unknown protein [Arabidopsis thaliana]

Seq. No. 401338
 Seq. ID LIB3431-042-P1-N1-B1
 Method BLASTX
 NCBI GI g4972067
 BLAST score 195
 E value 2.0e-15
 Match length 107
 % identity 50
 NCBI Description (AL078467) putative protei [Arabidopsis thaliana]

Seq. No. 401339
 Seq. ID LIB3431-042-P1-N1-B12
 Method BLASTX
 NCBI GI g729135
 BLAST score 315
 E value 7.0e-29
 Match length 74
 % identity 78
 NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE
 (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID
 3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir_S28612
 catechol O-methyltransferase (EC 2.1.1.6) - maize
 >gi_168532 (M73235) O-methyltransferase [Zea mays]

Seq. No. 401340
 Seq. ID LIB3431-042-P1-N1-B3
 Method BLASTX
 NCBI GI g3158476
 BLAST score 270
 E value 2.0e-23
 Match length 65
 % identity 75
 NCBI Description (AF067185) aquaporin 2 [Samanea saman]

Seq. No. 401341
 Seq. ID LIB3431-042-P1-N1-B4
 Method BLASTX
 NCBI GI g2065019
 BLAST score 258
 E value 3.0e-22
 Match length 95
 % identity 25
 NCBI Description (Y09823) hypothetical protein [Arabidopsis thaliana]

Seq. No. 401342
 Seq. ID LIB3431-042-P1-N1-B5
 Method BLASTX
 NCBI GI g871931
 BLAST score 161
 E value 8.0e-11

Match length 44
 % identity 75
 NCBI Description (D30763) ferredoxin [Oryza sativa]

Seq. No. 401343
 Seq. ID LIB3431-042-P1-N1-B6
 Method BLASTN
 NCBI GI g11957
 BLAST score 368
 E value 0.0e+00
 Match length 492
 % identity 95
 NCBI Description Rice complete chloroplast genome

Seq. No. 401344
 Seq. ID LIB3431-042-P1-N1-B8
 Method BLASTX
 NCBI GI g517500
 BLAST score 393
 E value 4.0e-38
 Match length 94
 % identity 82
 NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf_1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No. 401345
 Seq. ID LIB3431-042-P1-N1-B9
 Method BLASTX
 NCBI GI g517500
 BLAST score 421
 E value 2.0e-41
 Match length 112
 % identity 76
 NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf_1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No. 401346
 Seq. ID LIB3431-042-P1-N1-C1
 Method BLASTX
 NCBI GI g131225
 BLAST score 311
 E value 1.0e-28
 Match length 76
 % identity 76
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 401347
 Seq. ID LIB3431-042-P1-N1-C10
 Method BLASTX
 NCBI GI g2754849
 BLAST score 394
 E value 4.0e-38

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Match length      87
% identity        86
NCBI Description  (AF039000) putative serine-glyoxylate aminotransferase
                  [Fritillaria agrestis]
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Seq. No.          401348
Seq. ID           LIB3431-042-P1-N1-C11
Method            BLASTX
NCBI GI           g132105
BLAST score       421
E value           3.0e-41
Match length      76
% identity        100
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]

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Seq. No.	401349
Seq. ID	LIB3431-042-P1-N1-C4
Method	BLASTX
NCBI GI	g1483563
BLAST score	265
E value	6.0e-23
Match length	53
% identity	92
NCBI Description	(X99825) leucine aminopeptidase [Petroselinum crispum]

```
Seq. No.      401350
Seq. ID      LIB3431-042-P1-N1-C5
Method       BLASTX
NCBI GI      g671740
BLAST score   227
E value      1.0e-18
Match length  56
% identity    79
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
construct]
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```
Seq. No.      401351
Seq. ID       LIB3431-042-P1-N1-C6
Method        BLASTN
NCBI GI       g454881
BLAST score    207
E value       1.0e-113
Match length   234
% identity     97
NCBI Description  Rice gene for thioredoxin h, complete cds
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Seq. No.      401352
Seq. ID      LIB3431-042-P1-N1-C7
Method       BLASTX
```

NCBI GI g417260
 BLAST score 406
 E value 2.0e-39
 Match length 128
 % identity 65
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

Seq. No. 401353
 Seq. ID LIB3431-042-P1-N1-C9
 Method BLASTN
 NCBI GI g4079797
 BLAST score 66
 E value 1.0e-28
 Match length 246
 % identity 81
 NCBI Description Oryza sativa 23 kDa polypeptide of photosystem II mRNA,
 complete cds

Seq. No. 401354
 Seq. ID LIB3431-042-P1-N1-D10
 Method BLASTX
 NCBI GI g132105
 BLAST score 522
 E value 4.0e-53
 Match length 94
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 401355
 Seq. ID LIB3431-042-P1-N1-D11
 Method BLASTX
 NCBI GI g115787
 BLAST score 402
 E value 5.0e-39
 Match length 77
 % identity 99
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
 protein 2R precursor - rice >gi_20182_emb_CAA32109_
 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
 [Oryza sativa]

Seq. No. 401356
 Seq. ID LIB3431-042-P1-N1-D12
 Method BLASTN
 NCBI GI g452439
 BLAST score 68

E value 1.0e-17
 Match length 95
 % identity 47
 NCBI Description (AC009918) unknown protein [Arabidopsis thaliana]

Seq. No. 401362
 Seq. ID LIB3431-042-P1-N1-E2
 Method BLASTX
 NCBI GI g21839
 BLAST score 361
 E value 3.0e-34
 Match length 74
 % identity 96
 NCBI Description (X57952) phosphoribulokinase [Triticum aestivum]

Seq. No. 401363
 Seq. ID LIB3431-042-P1-N1-E3
 Method BLASTX
 NCBI GI g1173275
 BLAST score 653
 E value 2.0e-68
 Match length 147
 % identity 91
 NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S7
 >gi_2119068_pir_S58630 ribosomal protein S7 - maize
 chloroplast >gi_902274_emb_CAA60339 (X86563) ribosomal
 protein S7 [Zea mays] >gi_902298_emb_CAA60362 (X86563)
 ribosomal protein S7 [Zea mays]

Seq. No. 401364
 Seq. ID LIB3431-042-P1-N1-E5
 Method BLASTX
 NCBI GI g115787
 BLAST score 578
 E value 1.0e-59
 Match length 111
 % identity 100
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
 protein 2R precursor - rice >gi_20182_emb_CAA32109
 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
 [Oryza sativa]

Seq. No. 401365
 Seq. ID LIB3431-042-P1-N1-E6
 Method BLASTX
 NCBI GI g3582335
 BLAST score 191
 E value 2.0e-14
 Match length 62
 % identity 60
 NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]

Seq. No. 401366
 Seq. ID LIB3431-042-P1-N1-E7
 Method BLASTN
 NCBI GI g2072726

BLAST score 396
 E value 0.0e+00
 Match length 455
 % identity 97
 NCBI Description O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2

Seq. No. 401367
 Seq. ID LIB3431-042-P1-N1-E8
 Method BLASTX
 NCBI GI g671740
 BLAST score 320
 E value 1.0e-29
 Match length 61
 % identity 98
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 401368
 Seq. ID LIB3431-042-P1-N1-E9
 Method BLASTX
 NCBI GI g132105
 BLAST score 326
 E value 3.0e-30
 Match length 61
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401369
 Seq. ID LIB3431-042-P1-N1-F1
 Method BLASTX
 NCBI GI g671740
 BLAST score 233
 E value 3.0e-19
 Match length 47
 % identity 96
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 401370
 Seq. ID LIB3431-042-P1-N1-F10
 Method BLASTX
 NCBI GI g115813
 BLAST score 233
 E value 2.0e-19
 Match length 53
 % identity 85
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

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Seq. No.          401371
Seq. ID           LIB3431-042-P1-N1-F11
Method            BLASTN
NCBI GI           g2407280
BLAST score       44
E value           4.0e-16
Match length      56
% identity        95
NCBI Description   Oryza sativa ribulose 1,5-bisphosphate carboxylase small
                   subunit mRNA, complete cds

Seq. No.          401372
Seq. ID           LIB3431-042-P1-N1-F12
Method            BLASTX
NCBI GI           g733456
BLAST score       306
E value           6.0e-28
Match length      67
% identity        91
NCBI Description   (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
                   [Zea mays]

Seq. No.          401373
Seq. ID           LIB3431-042-P1-N1-F2
Method            BLASTX
NCBI GI           g548603
BLAST score       204
E value           2.0e-16
Match length      42
% identity        93
NCBI Description   PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                   >gi_478404_pir_JQ2247 photosystem I chain D precursor -
                   barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No.          401374
Seq. ID           LIB3431-042-P1-N1-F6
Method            BLASTX
NCBI GI           g3929924
BLAST score       298
E value           6.0e-27
Match length      56
% identity        100
NCBI Description   (AB020502) catalase [Oryza sativa]

Seq. No.          401375
Seq. ID           LIB3431-042-P1-N1-F7
Method            BLASTX
NCBI GI           g548603
BLAST score       562
E value           7.0e-58
Match length      110
% identity        97
NCBI Description   PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                   >gi_478404_pir_JQ2247 photosystem I chain D precursor -

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barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 401376
Seq. ID LIB3431-042-P1-N1-G1
Method BLASTX
NCBI GI g1353352
BLAST score 197
E value 4.0e-15
Match length 54
% identity 72
NCBI Description (U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No. 401377
Seq. ID LIB3431-042-P1-N1-G10
Method BLASTX
NCBI GI g3789954
BLAST score 174
E value 2.0e-12
Match length 31
% identity 100
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 401378
Seq. ID LIB3431-042-P1-N1-G11
Method BLASTN
NCBI GI g4680189
BLAST score 84
E value 3.0e-39
Match length 148
% identity 23
NCBI Description Oryza sativa subsp. indica putative dnaJ-like protein, putative myb-related protein, putative farnesyl pyrophosphate synthase, and hypothetical protein genes, complete cds

Seq. No. 401379
Seq. ID LIB3431-042-P1-N1-G2
Method BLASTX
NCBI GI g1708424
BLAST score 274
E value 4.0e-24
Match length 92
% identity 57
NCBI Description ISOFLAVONE REDUCTASE HOMOLOG >gi_1230614 (U48590) isoflavone reductase-like protein [Lupinus albus]

Seq. No. 401380
Seq. ID LIB3431-042-P1-N1-G3
Method BLASTN
NCBI GI g1658312
BLAST score 100
E value 9.0e-49
Match length 103
% identity 50
NCBI Description O.sativa osr40g2 gene

Seq. No. 401381
 Seq. ID LIB3431-042-P1-N1-G4
 Method BLASTX
 NCBI GI g132105
 BLAST score 295
 E value 1.0e-26
 Match length 57
 % identity 98
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401382
 Seq. ID LIB3431-042-P1-N1-G6
 Method BLASTX
 NCBI GI g3915088
 BLAST score 254
 E value 9.0e-22
 Match length 75
 % identity 63
 NCBI Description TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID 4-HYDROXYLASE) (CA4H) (C4H) (P450C4H) (CYTOCHROME P450 73) >gi_903872 (L38898) trans-cinnamate 4-monooxygenase [Petroselinum crispum]

Seq. No. 401383
 Seq. ID LIB3431-042-P1-N1-G8
 Method BLASTX
 NCBI GI g1617197
 BLAST score 276
 E value 3.0e-24
 Match length 71
 % identity 70
 NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 401384
 Seq. ID LIB3431-042-P1-N1-G9
 Method BLASTX
 NCBI GI g1617197
 BLAST score 189
 E value 3.0e-14
 Match length 39
 % identity 90
 NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 401385
 Seq. ID LIB3431-042-P1-N1-H1
 Method BLASTX
 NCBI GI g128191
 BLAST score 343

E value 4.0e-32
 Match length 73
 % identity 88
 NCBI Description NITRATE REDUCTASE [NAD(P)H] >gi_66210_pir_RDBHNP nitrate reductase (NAD(P)H) (EC 1.6.6.2) - barley
 >gi_19065_emb_CAA42739_(X60173) nitrate reductase (NAD(P)H) [Hordeum vulgare]

Seq. No. 401386
 Seq. ID LIB3431-042-P1-N1-H10
 Method BLASTN
 NCBI GI g3789953
 BLAST score 68
 E value 3.0e-30
 Match length 100
 % identity 92
 NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor (Cab26) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 401387
 Seq. ID LIB3431-042-P1-N1-H12
 Method BLASTN
 NCBI GI g5852077
 BLAST score 179
 E value 3.0e-96
 Match length 218
 % identity 96
 NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone: b6015

Seq. No. 401388
 Seq. ID LIB3431-042-P1-N1-H2
 Method BLASTN
 NCBI GI g169820
 BLAST score 90
 E value 7.0e-43
 Match length 373
 % identity 82
 NCBI Description Oryza sativa triosephosphate isomerase (Rictpi) mRNA, complete cds

Seq. No. 401389
 Seq. ID LIB3431-042-P1-N1-H3
 Method BLASTX
 NCBI GI g5734585
 BLAST score 307
 E value 5.0e-28
 Match length 82
 % identity 73
 NCBI Description (AJ245861) putative internal rotenone-insensitive NADH dehydrogenase [Solanum tuberosum]

Seq. No. 401390
 Seq. ID LIB3431-042-P1-N1-H7
 Method BLASTX
 NCBI GI g3914466

BLAST score 366
 E value 5.0e-35
 Match length 67
 % identity 97
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
 (PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN
 subunit precursor [Zea mays]

Seq. No. 401391
 Seq. ID LIB3431-043-P1-K1-A1
 Method BLASTX
 NCBI GI g132105
 BLAST score 735
 E value 4.0e-78
 Match length 156
 % identity 90
 NCBI Description RIBULOSE BISPHTOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 401392
 Seq. ID LIB3431-043-P1-K1-A11
 Method BLASTX
 NCBI GI g3126854
 BLAST score 628
 E value 1.0e-65
 Match length 119
 % identity 99
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401393
 Seq. ID LIB3431-043-P1-K1-A12
 Method BLASTN
 NCBI GI g3885887
 BLAST score 112
 E value 2.0e-56
 Match length 143
 % identity 96
 NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
 complete cds

Seq. No. 401394
 Seq. ID LIB3431-043-P1-K1-A2
 Method BLASTX
 NCBI GI g3150410
 BLAST score 277
 E value 2.0e-24
 Match length 96
 % identity 60
 NCBI Description (AC004165) unknown protein [Arabidopsis thaliana]

Seq. No. 401395
 Seq. ID LIB3431-043-P1-K1-A3
 Method BLASTX
 NCBI GI g3004555
 BLAST score 220
 E value 1.0e-17
 Match length 164
 % identity 12
 NCBI Description (AC003673) similar to salt inducible protein [Arabidopsis thaliana]

Seq. No. 401396
 Seq. ID LIB3431-043-P1-K1-A5
 Method BLASTN
 NCBI GI g4959460
 BLAST score 36
 E value 1.0e-10
 Match length 36
 % identity 100
 NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No. 401397
 Seq. ID LIB3431-043-P1-K1-A7
 Method BLASTX
 NCBI GI g125606
 BLAST score 184
 E value 2.0e-13
 Match length 59
 % identity 61
 NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir_S12248 pyruvate kinase (EC 2.7.1.40) - potato >gi_22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum tuberosum]

Seq. No. 401398
 Seq. ID LIB3431-043-P1-K1-A8
 Method BLASTX
 NCBI GI g3551954
 BLAST score 468
 E value 8.0e-47
 Match length 145
 % identity 57
 NCBI Description (AF082030) senescence-associated protein 5 [Hemerocallis hybrid cultivar]

Seq. No. 401399
 Seq. ID LIB3431-043-P1-K1-A9
 Method BLASTX
 NCBI GI g2570499
 BLAST score 191
 E value 1.0e-14
 Match length 38
 % identity 100
 NCBI Description (AF022732) 23kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 401400

Seq. ID LIB3431-043-P1-K1-B10
 Method BLASTX
 NCBI GI g132105
 BLAST score 690
 E value 8.0e-73
 Match length 147
 % identity 89
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401401
 Seq. ID LIB3431-043-P1-K1-B11
 Method BLASTX
 NCBI GI g2499417
 BLAST score 499
 E value 2.0e-50
 Match length 120
 % identity 78
 NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_1085826_pir_S49248 H-protein - Flaveria anomala >gi_547558_emb_CAA85761_ (Z37524) H-protein [Flaveria anomala]

Seq. No. 401402
 Seq. ID LIB3431-043-P1-K1-B2
 Method BLASTX
 NCBI GI g4079798
 BLAST score 537
 E value 7.0e-55
 Match length 104
 % identity 100
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 401403
 Seq. ID LIB3431-043-P1-K1-B3
 Method BLASTX
 NCBI GI g132105
 BLAST score 584
 E value 2.0e-60
 Match length 110
 % identity 97
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 401404
 Seq. ID LIB3431-043-P1-K1-B4
 Method BLASTX
 NCBI GI g3258238
 BLAST score 157
 E value 2.0e-10
 Match length 108
 % identity 30
 NCBI Description (AP000007) 224aa long hypothetical protein [Pyrococcus horikoshii]

Seq. No. 401405
 Seq. ID LIB3431-043-P1-K1-B5
 Method BLASTX
 NCBI GI g2982453
 BLAST score 224
 E value 3.0e-22
 Match length 72
 % identity 78
 NCBI Description (AL022223) fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana]

Seq. No. 401406
 Seq. ID LIB3431-043-P1-K1-B6
 Method BLASTX
 NCBI GI g132105
 BLAST score 839
 E value 3.0e-90
 Match length 175
 % identity 91
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401407
 Seq. ID LIB3431-043-P1-K1-B9
 Method BLASTX
 NCBI GI g732174
 BLAST score 531
 E value 3.0e-54
 Match length 144
 % identity 67
 NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE K03H1.2 >gi_3878176_emb_CAA82662.1_ (Z29560) similar to DEAH subfamily RNA helicases, especially yeast pre-mRNA splicing factors 22 and 16; cDNA EST EMBL:D27770 comes from this gene; cDNA EST EMBL:D27769 comes from this gene; cDNA EST EMBL:D36247 comes from thi... >gi_4249768_gb_AAD13795_ (AF120269) sex determination

096401a-101000

Seq. No.	401409
Seq. ID	LIB3431-043-P1-K1-C10
Method	BLASTN
NCBI GI	g21832
BLAST score	39
E value	1.0e-12
Match length	43
% identity	98
NCBI Description	Wheat mRNA for chloroplast phosphoglycerate kinase (EC 2.7.2.3)

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Seq. No.      401411
Seq. ID      LIB3431-043-P1-K1-C2
Method       BLASTX
NCBI GI      g115787
BLAST score   489
E value      2.0e-49
Match length  117
% identity    85
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Orvza sativa]
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51481

E value 5.0e-39
 Match length 163
 % identity 48
 NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No. 401418
 Seq. ID LIB3431-043-P1-K1-D10
 Method BLASTN
 NCBI GI g3618309
 BLAST score 157
 E value 3.0e-83
 Match length 173
 % identity 97
 NCBI Description Oryza sativa mRNA for zinc finger protein, complete cds, clone:E10707

Seq. No. 401419
 Seq. ID LIB3431-043-P1-K1-D12
 Method BLASTX
 NCBI GI g1718097
 BLAST score 448
 E value 2.0e-44
 Match length 125
 % identity 62
 NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT) (41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir_A55016 lysosomal membrane protein DVA41 - slime mold (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar ATPase subunit DVA41 [Dictyostelium discoideum]

Seq. No. 401420
 Seq. ID LIB3431-043-P1-K1-D2
 Method BLASTX
 NCBI GI g671740
 BLAST score 486
 E value 6.0e-49
 Match length 88
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 401421
 Seq. ID LIB3431-043-P1-K1-D3
 Method BLASTX
 NCBI GI g115787
 BLAST score 515
 E value 2.0e-52
 Match length 121
 % identity 86
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 401422
 Seq. ID LIB3431-043-P1-K1-D5

Method BLASTX
NCBI GI g417260
BLAST score 407
E value 1.0e-39
Match length 128
% identity 65
NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
light-regulated gene [Oryza sativa]

Seq. No. 401423
Seq. ID LIB3431-043-P1-K1-D7
Method BLASTX
NCBI GI g320618
BLAST score 530
E value 4.0e-54
Match length 121
% identity 83
NCBI Description chlorophyll a/b-binding protein I precursor - rice
>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
>gi_227611_prf_1707316A chlorophyll a/b binding protein 1
[Oryza sativa]

Seq. No. 401424
Seq. ID LIB3431-043-P1-K1-D8
Method BLASTX
NCBI GI g4583548
BLAST score 723
E value 1.0e-76
Match length 183
% identity 78
NCBI Description (AJ010820) chloroplast FtsY homolog [Arabidopsis thaliana]

Seq. No. 401425
Seq. ID LIB3431-043-P1-K1-D9
Method BLASTX
NCBI GI g1749676
BLAST score 147
E value 3.0e-09
Match length 82
% identity 44
NCBI Description (D89234) similar to Saccharomyces cerevisiae ORF YGR205W,
EMBL Accession Number Z72990 [Schizosaccharomyces pombe]

Seq. No. 401426
Seq. ID LIB3431-043-P1-K1-E1
Method BLASTN
NCBI GI g2773153
BLAST score 489
E value 0.0e+00
Match length 496
% identity 100
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
(Asr1) mRNA, complete cds

Seq. No. 401427

Seq. ID LIB3431-043-P1-K1-E10
 Method BLASTX
 NCBI GI g82080
 BLAST score 378
 E value 3.0e-36
 Match length 112
 % identity 66
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
 >gi_226872_prf_1609235A chlorophyll a/b binding protein
 [Lycopersicon esculentum]

Seq. No. 401428
 Seq. ID LIB3431-043-P1-K1-E12
 Method BLASTX
 NCBI GI g115787
 BLAST score 741
 E value 1.0e-78
 Match length 169
 % identity 88
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
 protein 2R precursor - rice >gi_20182_emb_CAA32109
 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
 [Oryza sativa]

Seq. No. 401429
 Seq. ID LIB3431-043-P1-K1-E3
 Method BLASTN
 NCBI GI g6006355
 BLAST score 221
 E value 1.0e-121
 Match length 297
 % identity 100
 NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No. 401430
 Seq. ID LIB3431-043-P1-K1-E5
 Method BLASTX
 NCBI GI g3256035
 BLAST score 238
 E value 9.0e-20
 Match length 135
 % identity 39
 NCBI Description (Y14274) putative serine/threonine protein kinase [Sorghum
 bicolor]

Seq. No. 401431
 Seq. ID LIB3431-043-P1-K1-E6
 Method BLASTX
 NCBI GI g3789954
 BLAST score 465
 E value 2.0e-46
 Match length 87
 % identity 98
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza
 sativa]

Seq. No. 401432
 Seq. ID LIB3431-043-P1-K1-E8
 Method BLASTX
 NCBI GI g729478
 BLAST score 413
 E value 2.0e-40
 Match length 158
 % identity 53
 NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
 >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
 reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_
 (AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to
 a region of the predicted gene.; similar to
 ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

Seq. No. 401433
 Seq. ID LIB3431-043-P1-K1-F12
 Method BLASTX
 NCBI GI g4585882
 BLAST score 721
 E value 2.0e-76
 Match length 159
 % identity 81
 NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein
 [Arabidopsis thaliana]

Seq. No. 401434
 Seq. ID LIB3431-043-P1-K1-F2
 Method BLASTX
 NCBI GI g2407281
 BLAST score 688
 E value 2.0e-72
 Match length 133
 % identity 97
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
 subunit [Oryza sativa]

Seq. No. 401435
 Seq. ID LIB3431-043-P1-K1-F6
 Method BLASTX
 NCBI GI g2443402
 BLAST score 824
 E value 2.0e-88
 Match length 162
 % identity 100
 NCBI Description (D87745) orthophosphate dikinase [Oryza sativa]
 >gi_2443405_dbj_BAA22420_ (D87952) orthophosphate dikinase
 [Oryza sativa]

Seq. No. 401436
 Seq. ID LIB3431-043-P1-K1-F8
 Method BLASTX
 NCBI GI g2739375
 BLAST score 150
 E value 2.0e-09
 Match length 95
 % identity 41

NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]

Seq. No. 401437
Seq. ID LIB3431-043-P1-K1-G1
Method BLASTX
NCBI GI g417488
BLAST score 580
E value 3.0e-72
Match length 155
% identity 85
NCBI Description ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE H) >gi_100452_pir_A40995 starch phosphorylase (EC 2.4.1.1) H - potato >gi_169473 (M69038) alpha-glucan phosphorylase type H isozyme [Solanum tuberosum]

Seq. No. 401438
Seq. ID LIB3431-043-P1-K1-G11
Method BLASTX
NCBI GI g3126854
BLAST score 581
E value 3.0e-60
Match length 109
% identity 100
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401439
Seq. ID LIB3431-043-P1-K1-G12
Method BLASTX
NCBI GI g131388
BLAST score 469
E value 7.0e-47
Match length 145
% identity 69
NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir_S16260 photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum aestivum]

Seq. No. 401440
Seq. ID LIB3431-043-P1-K1-G3
Method BLASTX
NCBI GI g3126854
BLAST score 671
E value 2.0e-76
Match length 144
% identity 99
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401441
Seq. ID LIB3431-043-P1-K1-G4
Method BLASTX
NCBI GI g5596468
BLAST score 266
E value 4.0e-23

Match length 82
 % identity 59
 NCBI Description (AL096882) putative protein [Arabidopsis thaliana]

Seq. No. 401442
 Seq. ID LIB3431-043-P1-K1-G5
 Method BLASTX
 NCBI GI g4454459
 BLAST score 564
 E value 5.0e-58
 Match length 133
 % identity 82
 NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 401443
 Seq. ID LIB3431-043-P1-K1-G7
 Method BLASTX
 NCBI GI g5091616
 BLAST score 643
 E value 3.0e-67
 Match length 202
 % identity 65
 NCBI Description (AC007454) F23M19.3 [Arabidopsis thaliana]

Seq. No. 401444
 Seq. ID LIB3431-043-P1-K1-G8
 Method BLASTX
 NCBI GI g115787
 BLAST score 586
 E value 1.0e-60
 Match length 133
 % identity 88
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 401445
 Seq. ID LIB3431-043-P1-K1-G9
 Method BLASTX
 NCBI GI g115787
 BLAST score 554
 E value 5.0e-57
 Match length 126
 % identity 87
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 401446
 Seq. ID LIB3431-043-P1-K1-H1
 Method BLASTX
 NCBI GI g5926718
 BLAST score 544

carboxylase (RuBPC) [Oryza sativa]

Seq. No. 401451
 Seq. ID LIB3431-043-P1-K1-H6
 Method BLASTX
 NCBI GI g3986110
 BLAST score 431
 E value 2.0e-42
 Match length 121
 % identity 69
 NCBI Description (AB012716) heat shock protein 70 cognate [Salix gilgiana]

Seq. No. 401452
 Seq. ID LIB3431-043-P1-K1-H8
 Method BLASTX
 NCBI GI g5669656
 BLAST score 273
 E value 6.0e-24
 Match length 98
 % identity 56
 NCBI Description (AF096263) ER33 protein [Lycopersicon esculentum]

Seq. No. 401453
 Seq. ID LIB3431-043-P1-N1-A11
 Method BLASTX
 NCBI GI g3126854
 BLAST score 300
 E value 3.0e-27
 Match length 57
 % identity 100
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401454
 Seq. ID LIB3431-043-P1-N1-A12
 Method BLASTN
 NCBI GI g3885887
 BLAST score 389
 E value 0.0e+00
 Match length 397
 % identity 99
 NCBI Description Oryza sativa high mobility group protein (HMG) mRNA, complete cds

Seq. No. 401455
 Seq. ID LIB3431-043-P1-N1-A4
 Method BLASTN
 NCBI GI g11957
 BLAST score 98
 E value 1.0e-47
 Match length 340
 % identity 41
 NCBI Description Rice complete chloroplast genome

Seq. No. 401456
 Seq. ID LIB3431-043-P1-N1-A9
 Method BLASTX
 NCBI GI g4079798

BLAST score 339
 E value 9.0e-32
 Match length 66
 % identity 98
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 401457
 Seq. ID LIB3431-043-P1-N1-B10
 Method BLASTX
 NCBI GI g132105
 BLAST score 508
 E value 1.0e-51
 Match length 91
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401458
 Seq. ID LIB3431-043-P1-N1-B11
 Method BLASTX
 NCBI GI g2499417
 BLAST score 309
 E value 3.0e-28
 Match length 71
 % identity 82
 NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_1085826_pir_S49248 H-protein - Flaveria anomala >gi_547558_emb_CAA85761_ (Z37524) H-protein [Flaveria anomala]

Seq. No. 401459
 Seq. ID LIB3431-043-P1-N1-B2
 Method BLASTX
 NCBI GI g4079798
 BLAST score 183
 E value 2.0e-13
 Match length 34
 % identity 100
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 401460
 Seq. ID LIB3431-043-P1-N1-B3
 Method BLASTX
 NCBI GI g347451
 BLAST score 248
 E value 4.0e-21
 Match length 48
 % identity 100

NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 401461
Seq. ID LIB3431-043-P1-N1-B4
Method BLASTN
NCBI GI g20262
BLAST score 191
E value 1.0e-103
Match length 379
% identity 88
NCBI Description O.sativa light-induced mRNA

Seq. No. 401462
Seq. ID LIB3431-043-P1-N1-B6
Method BLASTX
NCBI GI g132105
BLAST score 165
E value 2.0e-11
Match length 32
% identity 97
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401463
Seq. ID LIB3431-043-P1-N1-C1
Method BLASTX
NCBI GI g115787
BLAST score 409
E value 6.0e-40
Match length 77
% identity 100
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 401464
Seq. ID LIB3431-043-P1-N1-C12
Method BLASTN
NCBI GI g5360229
BLAST score 397
E value 0.0e+00
Match length 401
% identity 100
NCBI Description Oryza sativa mRNA for Ran, complete cds

Seq. No. 401465
Seq. ID LIB3431-043-P1-N1-C2

% identity 80
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_(X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 401476
Seq. ID LIB3431-043-P1-N1-E12
Method BLASTX
NCBI GI g3036946
BLAST score 271
E value 8.0e-24
Match length 52
% identity 98
NCBI Description (AB012637) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 401477
Seq. ID LIB3431-043-P1-N1-E3
Method BLASTN
NCBI GI g6006355
BLAST score 43
E value 7.0e-15
Match length 123
% identity 84
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No. 401478
Seq. ID LIB3431-043-P1-N1-E5
Method BLASTX
NCBI GI g3256035
BLAST score 195
E value 7.0e-15
Match length 67
% identity 55
NCBI Description (Y14274) putative serine/threonine protein kinase [Sorghum bicolor]

Seq. No. 401479
Seq. ID LIB3431-043-P1-N1-E7
Method BLASTX
NCBI GI g128690
BLAST score 535
E value 1.0e-54
Match length 118
% identity 89
NCBI Description NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 3, CHLOROPLAST >gi_66161_pir_DERZN3 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - rice chloroplast >gi_11989_emb_CAA34001_(X15901) ndhC; NADH dehydrogenase ND3 [Oryza sativa] >gi_226610_prf_1603356AG NADH dehydrogenase ND3 [Oryza sativa]

Seq. No. 401480
Seq. ID LIB3431-043-P1-N1-E8
Method BLASTN
NCBI GI g3819688
BLAST score 41

Match length 63
 % identity 89
 NCBI Description (AF039000) putative serine-glyoxylate aminotransferase
 [Fritillaria agrestis]

Seq. No. 401486
 Seq. ID LIB3431-043-P1-N1-G1
 Method BLASTX
 NCBI GI g417488
 BLAST score 152
 E value 4.0e-16
 Match length 51
 % identity 81
 NCBI Description ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE
 H) >gi_100452_pir_A40995 starch phosphorylase (EC 2.4.1.1)
 H - potato >gi_169473 (M69038) alpha-glucan phosphorylase
 type H isozyme [Solanum tuberosum]

Seq. No. 401487
 Seq. ID LIB3431-043-P1-N1-G10
 Method BLASTX
 NCBI GI g4006895
 BLAST score 158
 E value 3.0e-10
 Match length 51
 % identity 49
 NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 401488
 Seq. ID LIB3431-043-P1-N1-G11
 Method BLASTX
 NCBI GI g3126854
 BLAST score 277
 E value 2.0e-24
 Match length 52
 % identity 100
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401489
 Seq. ID LIB3431-043-P1-N1-G3
 Method BLASTX
 NCBI GI g3126854
 BLAST score 200
 E value 2.0e-19
 Match length 53
 % identity 98
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401490
 Seq. ID LIB3431-043-P1-N1-G4
 Method BLASTX
 NCBI GI g5596468
 BLAST score 145
 E value 5.0e-09
 Match length 43
 % identity 65
 NCBI Description (AL096882) putative protein [Arabidopsis thaliana]

Seq. No. 401496
 Seq. ID LIB3431-043-P1-N1-H3
 Method BLASTX
 NCBI GI g671740
 BLAST score 163
 E value 4.0e-11
 Match length 31
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 401497
 Seq. ID LIB3431-043-P1-N1-H4
 Method BLASTX
 NCBI GI g671740
 BLAST score 301
 E value 3.0e-27
 Match length 57
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 401498
 Seq. ID LIB3431-043-P1-N1-H5
 Method BLASTN
 NCBI GI g3218542
 BLAST score 36
 E value 1.0e-10
 Match length 119
 % identity 82
 NCBI Description Oryza sativa AOX1b and AOX1a genes, complete cds

Seq. No. 401499
 Seq. ID LIB3431-043-P1-N1-H6
 Method BLASTN
 NCBI GI g473216
 BLAST score 36
 E value 1.0e-10
 Match length 44
 % identity 95
 NCBI Description P.sativum (little marvel) HSC71.0 mRNA

Seq. No. 401500
 Seq. ID LIB3431-044-P1-K1-A1
 Method BLASTX
 NCBI GI g320618
 BLAST score 457
 E value 1.0e-45
 Match length 106
 % identity 83
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 401501

Seq. ID	LIB3431-044-P1-K1-A10
Method	BLASTX
NCBI GI	g3647283
BLAST score	278
E value	1.0e-45
Match length	147
% identity	63
NCBI Description	(AJ011418) ubiquitin activating enzyme [Lycopersicon esculentum]
Seq. No.	401502
Seq. ID	LIB3431-044-P1-K1-A11
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	8.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]
Seq. No.	401503
Seq. ID	LIB3431-044-P1-K1-A12
Method	BLASTX
NCBI GI	g2662343
BLAST score	815
E value	2.0e-87
Match length	159
% identity	98
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]
Seq. No.	401504
Seq. ID	LIB3431-044-P1-K1-A4
Method	BLASTX
NCBI GI	g1173275
BLAST score	653
E value	3.0e-74
Match length	150
% identity	96
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S7 >gi_2119068_pir_S58630 ribosomal protein S7 - maize chloroplast >gi_902274_emb_CAA60339_ (X86563) ribosomal protein S7 [Zea mays] >gi_902298_emb_CAA60362_ (X86563) ribosomal protein S7 [Zea mays]
Seq. No.	401505
Seq. ID	LIB3431-044-P1-K1-A5
Method	BLASTX
NCBI GI	g3126854
BLAST score	656
E value	5.0e-69
Match length	123
% identity	100
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.	401506

Seq. ID	LIB3431-044-P1-K1-A6
Method	BLASTX
NCBI GI	g1835731
BLAST score	594
E value	2.0e-61
Match length	126
% identity	91
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

```
Seq. No.      401507
Seq. ID      LIB3431-044-P1-K1-A7
Method       BLASTX
NCBI GI      g729477
BLAST score   603
E value      1.0e-62
Match length 126
% identity    87
NCBI Description  FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR)
                >gi_320548_pir_A44974 ferredoxin--NADP+ reductase (EC
                1.18.1.2) precursor - common ice plant >gi_167256 (M25528)
                ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1)
                [Mesembryanthemum crystallinum] >gi_226768_prf_1604475A
                ferredoxin NADP reductase [Mesembryanthemum crystallinum]
```

```
Seq. No.      401508
Seq. ID      LIB3431-044-P1-K1-A8
Method       BLASTX
NCBI GI      g3402711
BLAST score   349
E value      5.0e-33
Match length  120
% identity    57
NCBI Description (AC004261) putative RNA-binding protein [Arabidopsis thaliana]
```

```
Seq. No.      401509
Seq. ID       LIB3431-044-P1-K1-A9
Method        BLASTX
NCBI GI       g3789954
BLAST score    240
E value       2.0e-20
Match length   60
% identity     77
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza
sativa]
```

```
Seq. No.      401510
Seq. ID      LIB3431-044-P1-K1-B1
Method       BLASTX
NCBI GI      g2072555
BLAST score   237
E value      6.0e-20
Match length  44
% identity    100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
                >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                protein [Oryza sativa]
```

```
Seq. No.          401511
Seq. ID           LIB3431-044-P1-K1-B10
Method            BLASTX
NCBI GI           gi1731181
BLAST score       195
E value           7.0e-15
Match length      136
% identity        38
NCBI Description  HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II
                  >gi_3874230_emb_CAA90107.1_(Z49909) weak similarity with a
                  B. Flavum translocation protein (Swiss Prot accession
                  number P38376); cDNA EST yk220e10.5 comes from this gene;
                  cDNA EST yk549e12.3 comes from this gene; cDNA EST
                  yk618d6.3 comes from this gene
```

```
Seq. No.      401512
Seq. ID      LIB3431-044-P1-K1-B11
Method       BLASTX
NCBI GI      g3126854
BLAST score   717
E value      5.0e-76
Match length  137
% identity    99
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```

```
Seq. No.      401513
Seq. ID      LIB3431-044-P1-K1-B12
Method       BLASTX
NCBI GI      g548605
BLAST score   513
E value      4.0e-52
Match length  131
% identity    80
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                >gi_539055_pir_A48527 photosystem I protein psaK precursor
                - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                [Hordeum vulgare]
```

```
Seq. No.      401514
Seq. ID       LIB3431-044-P1-K1-B3
Method        BLASTX
NCBI GI       g4972093
BLAST score   227
E value       1.0e-18
Match length  131
% identity    40
NCBI Description (AL078468) putative protein [Arabidopsis thaliana]
```

```
Seq. No.          401515
Seq. ID           LIB3431-044-P1-K1-B4
Method            BLASTX
NCBI GI           g3063524
BLAST score       183
E value           2.0e-13
Match length      37
```

% identity 95
 NCBI Description (AF052305) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 401516
 Seq. ID LIB3431-044-P1-K1-B6
 Method BLASTN
 NCBI GI g6015437
 BLAST score 35
 E value 6.0e-10
 Match length 35
 % identity 100
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 401517
 Seq. ID LIB3431-044-P1-K1-B7
 Method BLASTX
 NCBI GI g2827150
 BLAST score 559
 E value 2.0e-57
 Match length 148
 % identity 76
 NCBI Description (AF029895) acetyl-coenzyme A carboxylase [Triticum aestivum]

Seq. No. 401518
 Seq. ID LIB3431-044-P1-K1-B8
 Method BLASTX
 NCBI GI g2344892
 BLAST score 213
 E value 7.0e-17
 Match length 68
 % identity 69
 NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]

Seq. No. 401519
 Seq. ID LIB3431-044-P1-K1-C1
 Method BLASTX
 NCBI GI g1495768
 BLAST score 152
 E value 8.0e-10
 Match length 144
 % identity 45
 NCBI Description (Z68506) chloroplast inner envelope protein, 110 kD (IEP110) [Pisum sativum]

Seq. No. 401520
 Seq. ID LIB3431-044-P1-K1-C10
 Method BLASTX
 NCBI GI g2130082
 BLAST score 442
 E value 1.0e-43
 Match length 169
 % identity 51
 NCBI Description protein kinase Xa21 (EC 2.7.1.-) - rice >gi_1122443 (U37133) receptor kinase-like protein [Oryza sativa] >gi_2586085 (U72723) receptor kinase-like protein [Oryza

longistaminata] >gi_1586408_prf_2203451A receptor
kinase-like protein [Oryza sativa]

Seq. No. 401521
Seq. ID LIB3431-044-P1-K1-C2
Method BLASTX
NCBI GI g2688824
BLAST score 181
E value 3.0e-13
Match length 111
% identity 41
NCBI Description (U93273) putative auxin-repressed protein [Prunus
armeniaca]

Seq. No. 401522
Seq. ID LIB3431-044-P1-K1-C3
Method BLASTX
NCBI GI g548603
BLAST score 295
E value 1.0e-26
Match length 56
% identity 98
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
(PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
>gi_478404_pir_JQ2247 photosystem I chain D precursor -
barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 401523
Seq. ID LIB3431-044-P1-K1-C9
Method BLASTX
NCBI GI g3789952
BLAST score 651
E value 2.0e-68
Match length 128
% identity 98
NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza
sativa]

Seq. No. 401524
Seq. ID LIB3431-044-P1-K1-D1
Method BLASTX
NCBI GI g399213
BLAST score 877
E value 1.0e-94
Match length 181
% identity 96
NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG
CD4B PRECURSOR >gi_100190_pir_B35905 CD4B protein - tomato
>gi_170435 (M32604) ATP-dependent protease (CD4B)
[Lycopersicon esculentum]

Seq. No. 401525
Seq. ID LIB3431-044-P1-K1-D12
Method BLASTN
NCBI GI g5295936
BLAST score 46
E value 2.0e-16

Match length 93
 % identity 85
 NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0681F10,
 complete sequence

Seq. No. 401526
 Seq. ID LIB3431-044-P1-K1-D2
 Method BLASTX
 NCBI GI g2492515
 BLAST score 662
 E value 2.0e-69
 Match length 155
 % identity 86
 NCBI Description CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
 >gi_2129924_pir_S58298 ATPase - pepper (fragment)
 >gi_929013_emb_CAA62084_ (X90472) ATPase [Capsicum annuum]

Seq. No. 401527
 Seq. ID LIB3431-044-P1-K1-D6
 Method BLASTX
 NCBI GI g1652164
 BLAST score 490
 E value 3.0e-49
 Match length 167
 % identity 61
 NCBI Description (D90903) hypothetical protein [Synecocystis sp.]

Seq. No. 401528
 Seq. ID LIB3431-044-P1-K1-E10
 Method BLASTX
 NCBI GI g3618310
 BLAST score 439
 E value 3.0e-43
 Match length 132
 % identity 69
 NCBI Description (AB001883) zinc finger protein [Oryza sativa]

Seq. No. 401529
 Seq. ID LIB3431-044-P1-K1-E11
 Method BLASTX
 NCBI GI g3126854
 BLAST score 784
 E value 8.0e-84
 Match length 151
 % identity 97
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401530
 Seq. ID LIB3431-044-P1-K1-E12
 Method BLASTX
 NCBI GI g131225
 BLAST score 670
 E value 2.0e-70
 Match length 151
 % identity 88
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
 V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein

precursor - barley >gi_167087 (M61146) photosystem I
hydrophobic protein [*Hordeum vulgare*]

Seq. No. 401531
Seq. ID LIB3431-044-P1-K1-E5
Method BLASTX
NCBI GI g115787
BLAST score 762
E value 3.0e-81
Match length 149
% identity 99
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
protein 2R precursor - rice >gi_20182_emb_CAA32109
(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
[*Oryza sativa*]

Seq. No. 401532
Seq. ID LIB3431-044-P1-K1-E6
Method BLASTX
NCBI GI g5042409
BLAST score 442
E value 1.0e-43
Match length 136
% identity 64
NCBI Description (AC006193) Putative membrane related protein [*Arabidopsis*
thaliana]

Seq. No. 401533
Seq. ID LIB3431-044-P1-K1-E7
Method BLASTX
NCBI GI g5702231
BLAST score 190
E value 3.0e-14
Match length 108
% identity 44
NCBI Description (AF145386) hypersensitive reaction associated Ca²⁺-binding
protein [*Phaseolus vulgaris*]

Seq. No. 401534
Seq. ID LIB3431-044-P1-K1-E8
Method BLASTX
NCBI GI g548605
BLAST score 590
E value 5.0e-61
Match length 130
% identity 90
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
>gi_539055_pir_A48527 photosystem I protein psaK precursor
- barley >gi_304220 (L12707) photosystem I PSI-K subunit
[*Hordeum vulgare*]

Seq. No. 401535
Seq. ID LIB3431-044-P1-K1-E9
Method BLASTN
NCBI GI g3821780

E value 1.0e-81
 Match length 170
 % identity 85
 NCBI Description homeotic protein - Phalaenopsis sp >gi_1173622 (U34743)
 homeobox protein [Phalaenopsis sp. 'hybrid SM9108']

Seq. No. 401541
 Seq. ID LIB3431-044-P1-K1-F6
 Method BLASTX
 NCBI GI g1644427
 BLAST score 452
 E value 7.0e-45
 Match length 130
 % identity 66
 NCBI Description (U74610) glyoxalase II [Arabidopsis thaliana]

Seq. No. 401542
 Seq. ID LIB3431-044-P1-K1-F7
 Method BLASTX
 NCBI GI g1617197
 BLAST score 301
 E value 3.0e-27
 Match length 76
 % identity 75
 NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 401543
 Seq. ID LIB3431-044-P1-K1-F8
 Method BLASTX
 NCBI GI g2072555
 BLAST score 218
 E value 2.0e-17
 Match length 44
 % identity 93
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 401544
 Seq. ID LIB3431-044-P1-K1-F9
 Method BLASTX
 NCBI GI g1352461
 BLAST score 388
 E value 2.0e-37
 Match length 90
 % identity 83
 NCBI Description IN2-2 PROTEIN

Seq. No. 401545
 Seq. ID LIB3431-044-P1-K1-G1
 Method BLASTX
 NCBI GI g4972067
 BLAST score 287
 E value 2.0e-27
 Match length 166
 % identity 44
 NCBI Description (AL078467) putative protei [Arabidopsis thaliana]

```
Seq. No.      401546
Seq. ID      LIB3431-044-P1-K1-G10
Method       BLASTX
NCBI GI      g3132476
BLAST score   579
E value      9.0e-60
Match length  167
% identity    66
NCBI Description (AC003096) unknown protein [Arabidopsis thaliana]
```

```
Seq. No.      401547
Seq. ID      LIB3431-044-P1-K1-G11
Method       BLASTX
NCBI GI      g320618
BLAST score   616
E value      4.0e-64
Match length  134
% identity    87
NCBI Description  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_(D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
```

```
Seq. No.      401548
Seq. ID      LIB3431-044-P1-K1-G12
Method       BLASTX
NCBI GI      g4490728
BLAST score   290
E value      6.0e-26
Match length  65
% identity    75
NCBI Description (AL035709) putative protein [Arabidopsis thaliana]
```

Seq. No.	401549
Seq. ID	LIB3431-044-P1-K1-G3
Method	BLASTN
NCBI GI	g19094
BLAST score	48
E value	4.0e-18
Match length	64
% identity	94
NCBI Description	H.vulgare mRNA PsaN for photosystem I subunit N

```
Seq. No.      401550
Seq. ID      LIB3431-044-P1-K1-G4
Method       BLASTX
NCBI GI      g1684851
BLAST score   212
E value      6.0e-17
Match length  62
% identity    68
NCBI Description (U77935) DnaJ-like protein [Phaseolus vulgaris]
```

Seq. No.	401551
Seq. ID	LIB3431-044-P1-K1-G6

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 401561
 Seq. ID LIB3431-044-P1-K1-H9
 Method BLASTX
 NCBI GI g132105
 BLAST score 830
 E value 4.0e-89
 Match length 173
 % identity 91
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 401562
 Seq. ID LIB3431-044-P1-N1-A1
 Method BLASTN
 NCBI GI g218171
 BLAST score 58
 E value 2.0e-24
 Match length 84
 % identity 93
 NCBI Description Oryza sativa mRNA for type I light-harvesting chlorophyll
 a/b binding protein of photosystem II (LHCPII), complete
 cds

Seq. No. 401563
 Seq. ID LIB3431-044-P1-N1-A10
 Method BLASTX
 NCBI GI g2982309
 BLAST score 194
 E value 8.0e-15
 Match length 46
 % identity 78
 NCBI Description (AF051239) probable ubiquitin activating enzyme 2 [Picea
 mariana]

Seq. No. 401564
 Seq. ID LIB3431-044-P1-N1-A11
 Method BLASTN
 NCBI GI g2072554
 BLAST score 240
 E value 1.0e-132
 Match length 248

% identity 99
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 401565
Seq. ID LIB3431-044-P1-N1-A12
Method BLASTN
NCBI GI g2662340
BLAST score 59
E value 8.0e-25
Match length 91
% identity 91
NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds

Seq. No. 401566
Seq. ID LIB3431-044-P1-N1-A4
Method BLASTX
NCBI GI g1173275
BLAST score 640
E value 7.0e-67
Match length 149
% identity 89
NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S7
>gi_2119068_pir_S58630 ribosomal protein S7 - maize
chloroplast >gi_902274_emb_CAA60339_ (X86563) ribosomal
protein S7 [Zea mays] >gi_902298_emb_CAA60362_ (X86563)
ribosomal protein S7 [Zea mays]

Seq. No. 401567
Seq. ID LIB3431-044-P1-N1-A5
Method BLASTN
NCBI GI g2570512
BLAST score 88
E value 8.0e-42
Match length 195
% identity 96
NCBI Description Oryza sativa chlorophyll a-b binding protein mRNA, complete cds

Seq. No. 401568
Seq. ID LIB3431-044-P1-N1-A6
Method BLASTX
NCBI GI g1835731
BLAST score 436
E value 4.0e-43
Match length 94
% identity 89
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 401569
Seq. ID LIB3431-044-P1-N1-A7
Method BLASTN
NCBI GI g1835730
BLAST score 51
E value 3.0e-20
Match length 59
% identity 97

NCBI Description Oryza sativa photosystem II 10 kDa polypeptide mRNA, complete cds

Seq. No. 401570
 Seq. ID LIB3431-044-P1-N1-A9
 Method BLASTN
 NCBI GI g3789953
 BLAST score 267
 E value 1.0e-148
 Match length 275
 % identity 99

NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor (Cab26) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 401571
 Seq. ID LIB3431-044-P1-N1-B1
 Method BLASTN
 NCBI GI g2072554
 BLAST score 113
 E value 5.0e-57
 Match length 164
 % identity 93

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 401572
 Seq. ID LIB3431-044-P1-N1-B11
 Method BLASTX
 NCBI GI g3126854
 BLAST score 410
 E value 4.0e-40
 Match length 78
 % identity 99

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401573
 Seq. ID LIB3431-044-P1-N1-B12
 Method BLASTX
 NCBI GI g548605
 BLAST score 187
 E value 2.0e-14
 Match length 38
 % identity 95

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir_A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No. 401574
 Seq. ID LIB3431-044-P1-N1-B2
 Method BLASTN
 NCBI GI g19086
 BLAST score 56
 E value 1.0e-22
 Match length 100

% identity 91
NCBI Description Hordeum vulgare pot. psaE mRNA

Seq. No. 401575
Seq. ID LIB3431-044-P1-N1-B8
Method BLASTX
NCBI GI g2344892
BLAST score 182
E value 2.0e-13
Match length 41
% identity 80
NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]

Seq. No. 401576
Seq. ID LIB3431-044-P1-N1-C11
Method BLASTN
NCBI GI g1777706
BLAST score 59
E value 1.0e-24
Match length 71
% identity 96
NCBI Description Zea mays 18S ribosomal RNA gene, partial sequence

Seq. No. 401577
Seq. ID LIB3431-044-P1-N1-C4
Method BLASTX
NCBI GI g2829916
BLAST score 297
E value 7.0e-27
Match length 72
% identity 78
NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No. 401578
Seq. ID LIB3431-044-P1-N1-C9
Method BLASTN
NCBI GI g3789951
BLAST score 157
E value 6.0e-83
Match length 300
% identity 93
NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 401579
Seq. ID LIB3431-044-P1-N1-D6
Method BLASTX
NCBI GI g1652164
BLAST score 145
E value 6.0e-09
Match length 59
% identity 51
NCBI Description (D90903) hypothetical protein [Synechocystis sp.]

Seq. No. 401580
Seq. ID LIB3431-044-P1-N1-E10

Seq. No. 401585
Seq. ID LIB3431-044-P1-N1-F3
Method BLASTN
NCBI GI g20181
BLAST score 76
E value 1.0e-34
Match length 118
% identity 94
NCBI Description Rice cab2R gene for light harvesting chlorophyll
a/b-binding protein

Seq. No. 401586
Seq. ID LIB3431-044-P1-N1-F6
Method BLASTX
NCBI GI g1644427
BLAST score 343
E value 3.0e-32
Match length 79
% identity 80
NCBI Description (U74610) glyoxalase II [Arabidopsis thaliana]

Seq. No. 401587
Seq. ID LIB3431-044-P1-N1-F7
Method BLASTX
NCBI GI g1617197
BLAST score 148
E value 2.0e-09
Match length 30
% identity 87
NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 401588
Seq. ID LIB3431-044-P1-N1-F8
Method BLASTN
NCBI GI g2072554
BLAST score 209
E value 1.0e-114
Match length 265
% identity 97
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
cds

Seq. No. 401589
Seq. ID LIB3431-044-P1-N1-F9
Method BLASTX
NCBI GI g2462750
BLAST score 204
E value 6.0e-16
Match length 58
% identity 67
NCBI Description (AC002292) Highly similar to auxin-induced protein
(aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 401590
Seq. ID LIB3431-044-P1-N1-G11
Method BLASTX
NCBI GI g115787

BLAST score 389
 E value 1.0e-37
 Match length 75
 % identity 99
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 401591
 Seq. ID LIB3431-044-P1-N1-G6
 Method BLASTX
 NCBI GI g1052960
 BLAST score 224
 E value 3.0e-18
 Match length 54
 % identity 81
 NCBI Description (U37437) PNIL34 [Ipomoea nil]

Seq. No. 401592
 Seq. ID LIB3431-044-P1-N1-G9
 Method BLASTX
 NCBI GI g2072555
 BLAST score 307
 E value 5.0e-28
 Match length 55
 % identity 98
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 401593
 Seq. ID LIB3431-044-P1-N1-H12
 Method BLASTX
 NCBI GI g4996602
 BLAST score 268
 E value 2.0e-23
 Match length 71
 % identity 75
 NCBI Description (AB022273) thylakoid-bound ascorbate peroxidase [Nicotiana tabacum]

Seq. No. 401594
 Seq. ID LIB3431-044-P1-N1-H2
 Method BLASTN
 NCBI GI g2072726
 BLAST score 430
 E value 0.0e+00
 Match length 468
 % identity 98
 NCBI Description O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2

Seq. No. 401595
 Seq. ID LIB3431-044-P1-N1-H3
 Method BLASTN
 NCBI GI g2570514

indica]

Seq. No. 401600
Seq. ID LIB3431-045-P1-K1-A10
Method BLASTN
NCBI GI g5441876
BLAST score 106
E value 2.0e-52
Match length 327
% identity 35
NCBI Description Oryza sativa genomic DNA, chromosome 2, clone:P0437H03
(contig b)

Seq. No. 401601
Seq. ID LIB3431-045-P1-K1-A12
Method BLASTX
NCBI GI g4689380
BLAST score 640
E value 5.0e-67
Match length 139
% identity 83
NCBI Description (AF139465) LHCII type III chlorophyll a/b binding protein
[Vigna radiata]

Seq. No. 401602
Seq. ID LIB3431-045-P1-K1-A3
Method BLASTX
NCBI GI g132105
BLAST score 752
E value 4.0e-80
Match length 160
% identity 90
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 401603
Seq. ID LIB3431-045-P1-K1-A4
Method BLASTX
NCBI GI g132105
BLAST score 794
E value 5.0e-85
Match length 168
% identity 90
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

sativa] >gi_226375_prf_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 401604
Seq. ID LIB3431-045-P1-K1-A5
Method BLASTX
NCBI GI g4581146
BLAST score 587
E value 7.0e-61
Match length 142
% identity 82
NCBI Description (AC006919) putative fructose-bisphosphate aldolase,
cytoplasmic [Arabidopsis thaliana]

Seq. No. 401605
Seq. ID LIB3431-045-P1-K1-A6
Method BLASTX
NCBI GI g2407281
BLAST score 814
E value 2.0e-87
Match length 154
% identity 99
NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
subunit [Oryza sativa]

Seq. No. 401606
Seq. ID LIB3431-045-P1-K1-A7
Method BLASTX
NCBI GI g871931
BLAST score 517
E value 2.0e-52
Match length 131
% identity 80
NCBI Description (D30763) ferredoxin [Oryza sativa]

Seq. No. 401607
Seq. ID LIB3431-045-P1-K1-A8
Method BLASTX
NCBI GI g115787
BLAST score 654
E value 1.0e-68
Match length 127
% identity 98
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
protein 2R precursor - rice >gi_20182_emb_CAA32109
(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
[Oryza sativa]

Seq. No. 401608
Seq. ID LIB3431-045-P1-K1-B1
Method BLASTX
NCBI GI g3885886
BLAST score 502
E value 8.0e-51
Match length 120
% identity 80

% identity 81
 NCBI Description (AC009525) Unknown protein [Arabidopsis thaliana]
 Seq. No. 401614
 Seq. ID LIB3431-045-P1-K1-B6
 Method BLASTX
 NCBI GI g2191152
 BLAST score 222
 E value 8.0e-18
 Match length 117
 % identity 50
 NCBI Description (AF007269) A_IG002N01.31 gene product [Arabidopsis thaliana]

Seq. No. 401615
 Seq. ID LIB3431-045-P1-K1-B7
 Method BLASTX
 NCBI GI g1495768
 BLAST score 329
 E value 2.0e-30
 Match length 149
 % identity 46
 NCBI Description (Z68506) chloroplast inner envelope protein, 110 kD (IEP110) [Pisum sativum]

Seq. No. 401616
 Seq. ID LIB3431-045-P1-K1-B8
 Method BLASTX
 NCBI GI g132105
 BLAST score 690
 E value 8.0e-73
 Match length 147
 % identity 89
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401617
 Seq. ID LIB3431-045-P1-K1-B9
 Method BLASTX
 NCBI GI g3169012
 BLAST score 485
 E value 1.0e-48
 Match length 123
 % identity 76
 NCBI Description (AJ002610) putative calmodulin binding transporter protein [Hordeum vulgare]

Seq. No. 401618
 Seq. ID LIB3431-045-P1-K1-C1
 Method BLASTX

NCBI GI g320618
 BLAST score 356
 E value 8.0e-34
 Match length 84
 % identity 81
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 401619
 Seq. ID LIB3431-045-P1-K1-C10
 Method BLASTX
 NCBI GI g3885894
 BLAST score 551
 E value 1.0e-56
 Match length 136
 % identity 80
 NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No. 401620
 Seq. ID LIB3431-045-P1-K1-C2
 Method BLASTX
 NCBI GI g444790
 BLAST score 255
 E value 7.0e-22
 Match length 124
 % identity 52
 NCBI Description nucleotide translocator [Arabidopsis thaliana]

Seq. No. 401621
 Seq. ID LIB3431-045-P1-K1-C9
 Method BLASTN
 NCBI GI g2306980
 BLAST score 37
 E value 7.0e-12
 Match length 41
 % identity 98
 NCBI Description Oryza sativa photosystem I antenna protein (Lhca) mRNA,
 complete cds

Seq. No. 401622
 Seq. ID LIB3431-045-P1-K1-D11
 Method BLASTX
 NCBI GI g2497903
 BLAST score 220
 E value 9.0e-18
 Match length 59
 % identity 68
 NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2
 >gi_1752831_dbj_BAA14038.1 (D89931) metallothionein-like
 protein [Oryza sativa] >gi_1815628 (U43530)
 metallothionein-like type 2 [Oryza sativa]

Seq. No. 401623
 Seq. ID LIB3431-045-P1-K1-D12

Method BLASTX
 NCBI GI g1174780
 BLAST score 534
 E value 1.0e-54
 Match length 113
 % identity 88
 NCBI Description TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR (ORANGE PERICARP 2) >gi_320135_pir_PQ0450 tryptophan synthase (EC 4.2.1.20) beta-2 chain precursor - maize (fragment) >gi_168574 (M76685) tryptophan synthase beta-subunit [Zea mays]

Seq. No. 401624
 Seq. ID LIB3431-045-P1-K1-D3
 Method BLASTX
 NCBI GI g5051771
 BLAST score 293
 E value 3.0e-26
 Match length 96
 % identity 66
 NCBI Description (AL078637) putative protein [Arabidopsis thaliana]

Seq. No. 401625
 Seq. ID LIB3431-045-P1-K1-D5
 Method BLASTX
 NCBI GI g132105
 BLAST score 511
 E value 6.0e-52
 Match length 115
 % identity 85
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401626
 Seq. ID LIB3431-045-P1-K1-D6
 Method BLASTX
 NCBI GI g2072555
 BLAST score 175
 E value 2.0e-12
 Match length 32
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 401627
 Seq. ID LIB3431-045-P1-K1-D8
 Method BLASTX
 NCBI GI g115787
 BLAST score 717
 E value 4.0e-76

% identity 66
 NCBI Description (AF134121) Lhca5 protein [Arabidopsis thaliana]

Seq. No. 401633
 Seq. ID LIB3431-045-P1-K1-E4
 Method BLASTX
 NCBI GI g3075488
 BLAST score 429
 E value 2.0e-42
 Match length 107
 % identity 79
 NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 401634
 Seq. ID LIB3431-045-P1-K1-E6
 Method BLASTN
 NCBI GI g5042437
 BLAST score 58
 E value 1.0e-23
 Match length 97
 % identity 90
 NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence

Seq. No. 401635
 Seq. ID LIB3431-045-P1-K1-E9
 Method BLASTX
 NCBI GI g131225
 BLAST score 609
 E value 3.0e-63
 Match length 148
 % identity 79
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 401636
 Seq. ID LIB3431-045-P1-K1-F1
 Method BLASTX
 NCBI GI g3212852
 BLAST score 523
 E value 4.0e-53
 Match length 174
 % identity 60
 NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 401637
 Seq. ID LIB3431-045-P1-K1-F11
 Method BLASTX
 NCBI GI g5733866
 BLAST score 514
 E value 3.0e-52
 Match length 153
 % identity 63
 NCBI Description (AC007932) Contains similarity to gb_M73488 1-aminocyclopropane-1-carboxylate deaminase from Pseudomonas sp. ESTs gb_Z18033 and gb_Z34214 come from

Seq. ID	LIB3431-045-P1-K1-F9
Method	BLASTX
NCBI GI	g5734636
BLAST score	385
E value	5.0e-37
Match length	138
% identity	51
NCBI Description	(AP000391) Similar to putative lipase (AC006232) [Oryza sativa]
Seq. No.	401644
Seq. ID	LIB3431-045-P1-K1-G1
Method	BLASTX
NCBI GI	g2129538
BLAST score	618
E value	2.0e-64
Match length	132
% identity	89
NCBI Description	AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232) AT103 [Arabidopsis thaliana]
Seq. No.	401645
Seq. ID	LIB3431-045-P1-K1-G12
Method	BLASTX
NCBI GI	g3914603
BLAST score	836
E value	6.0e-90
Match length	161
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]
Seq. No.	401646
Seq. ID	LIB3431-045-P1-K1-G2
Method	BLASTX
NCBI GI	g3914603
BLAST score	881
E value	4.0e-95
Match length	169
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]
Seq. No.	401647
Seq. ID	LIB3431-045-P1-K1-G3
Method	BLASTX
NCBI GI	g3928083
BLAST score	522
E value	4.0e-53
Match length	138
% identity	70
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

0001016-101000

Seq. No. 401648
 Seq. ID LIB3431-045-P1-K1-G5
 Method BLASTX
 NCBI GI g4006881
 BLAST score 312
 E value 7.0e-37
 Match length 120
 % identity 67
 NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 401649
 Seq. ID LIB3431-045-P1-K1-G6
 Method BLASTX
 NCBI GI g3914005
 BLAST score 470
 E value 5.0e-47
 Match length 105
 % identity 90
 NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_1816586 (U85494) LON1 protease [Zea mays]

Seq. No. 401650
 Seq. ID LIB3431-045-P1-K1-G8
 Method BLASTX
 NCBI GI g2570515
 BLAST score 244
 E value 2.0e-21
 Match length 92
 % identity 68
 NCBI Description (AF022740) glycolate oxidase [Oryza sativa]

Seq. No. 401651
 Seq. ID LIB3431-045-P1-K1-H10
 Method BLASTX
 NCBI GI g3789952
 BLAST score 207
 E value 2.0e-16
 Match length 41
 % identity 95
 NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No. 401652
 Seq. ID LIB3431-045-P1-K1-H11
 Method BLASTN
 NCBI GI g2331130
 BLAST score 222
 E value 1.0e-121
 Match length 226
 % identity 100
 NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds

Seq. No. 401653
 Seq. ID LIB3431-045-P1-K1-H12
 Method BLASTX
 NCBI GI g3510256

E value 2.0e-27
 Match length 58
 % identity 100
 NCBI Description (AB012638) light harvesting chlorophyll a/b-binding protein
 [Nicotiana sylvestris]

Seq. No. 401659
 Seq. ID LIB3431-045-P1-N1-A10
 Method BLASTN
 NCBI GI g5441876
 BLAST score 390
 E value 0.0e+00
 Match length 454
 % identity 96
 NCBI Description Oryza sativa genomic DNA, chromosome 2, clone:P0437H03
 (contig b)

Seq. No. 401660
 Seq. ID LIB3431-045-P1-N1-A2
 Method BLASTX
 NCBI GI g1070408
 BLAST score 174
 E value 2.0e-12
 Match length 47
 % identity 77
 NCBI Description ferredoxin [2Fe-2S] I - rice

Seq. No. 401661
 Seq. ID LIB3431-045-P1-N1-A3
 Method BLASTX
 NCBI GI g347451
 BLAST score 326
 E value 3.0e-30
 Match length 61
 % identity 100
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
 sativa]

Seq. No. 401662
 Seq. ID LIB3431-045-P1-N1-A4
 Method BLASTX
 NCBI GI g671740
 BLAST score 301
 E value 2.0e-27
 Match length 57
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
 construct]

Seq. No. 401663
 Seq. ID LIB3431-045-P1-N1-A5
 Method BLASTX
 NCBI GI g5419990
 BLAST score 204
 E value 5.0e-16
 Match length 66
 % identity 62

NCBI Description (AJ243524) putative fructose-bisphosphate aldolase [Phleum pratense]

```
Seq. No.          401664
Seq. ID           LIB3431-045-P1-N1-A6
Method            BLASTX
NCBI GI           g347451
BLAST score       207
E value           3.0e-16
Match length      39
% identity         100
NCBI Description   (L22155) ribulose 1,
                   sativa]
```

```
Seq. No.          401665
Seq. ID           LIB3431-045-P1-N1-A7
Method            BLASTN
NCBI GI           g5670155
BLAST score       113
E value           1.0e-56
Match length      353
% identity        88
NCBI Description   Oryza sativa subsp. japonica BAC clone 34K24, complete
                   sequence
```

```
Seq. No.      401666
Seq. ID      LIB3431-045-P1-N1-A8
Method       BLASTX
NCBI GI      g115791
BLAST score   194
E value      8.0e-15
Match length  44
% identity   82
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_81770_pir_S01961 chlorophyll a/b-binding
                  protein 2 precursor - soybean >gi_18548_emb_CAA31418_
                  (X12980) chlorophyll a/b binding preprotein (AA -33 to 223)
                  [Glycine max]
```

Seq. No.	401667
Seq. ID	LIB3431-045-P1-N1-B1
Method	BLASTX
NCBI GI	g3885886
BLAST score	163
E value	4.0e-11
Match length	32
% identity	84
NCBI Description	(AF093631) Rieske Fe-S precursor protein [Oryza sativa]

```
Seq. No.          401668
Seq. ID           LIB3431-045-P1-N1-B10
Method            BLASTX
NCBI GI           g3549656
BLAST score       177
E value           9.0e-13
Match length      75
% identity        45
```

NCBI Description (AL031394) putative protein [Arabidopsis thaliana]

Seq. No. 401669
 Seq. ID LIB3431-045-P1-N1-B12
 Method BLASTX
 NCBI GI g3892058
 BLAST score 267
 E value 3.0e-23
 Match length 82
 % identity 56
 NCBI Description (AC002330) putative glutamate-/aspartate-binding peptide [Arabidopsis thaliana]

Seq. No. 401670
 Seq. ID LIB3431-045-P1-N1-B2
 Method BLASTN
 NCBI GI g2662342
 BLAST score 58
 E value 7.0e-24
 Match length 89
 % identity 95
 NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds

Seq. No. 401671
 Seq. ID LIB3431-045-P1-N1-B4
 Method BLASTX
 NCBI GI g132105
 BLAST score 302
 E value 2.0e-27
 Match length 58
 % identity 98
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401672
 Seq. ID LIB3431-045-P1-N1-B8
 Method BLASTX
 NCBI GI g671740
 BLAST score 277
 E value 2.0e-24
 Match length 53
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 401673
 Seq. ID LIB3431-045-P1-N1-C1
 Method BLASTN
 NCBI GI g2306980
 BLAST score 50

E value 3.0e-19
 Match length 70
 % identity 93
 NCBI Description Oryza sativa photosystem I antenna protein (Lhca) mRNA,
 complete cds

Seq. No. 401674
 Seq. ID LIB3431-045-P1-N1-C10
 Method BLASTX
 NCBI GI g3885894
 BLAST score 213
 E value 5.0e-17
 Match length 66
 % identity 65
 NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No. 401675
 Seq. ID LIB3431-045-P1-N1-C12
 Method BLASTN
 NCBI GI g20181
 BLAST score 79
 E value 3.0e-36
 Match length 107
 % identity 93
 NCBI Description Rice cab2R gene for light harvesting chlorophyll
 a/b-binding protein

Seq. No. 401676
 Seq. ID LIB3431-045-P1-N1-C9
 Method BLASTN
 NCBI GI g2306980
 BLAST score 87
 E value 4.0e-41
 Match length 175
 % identity 86
 NCBI Description Oryza sativa photosystem I antenna protein (Lhca) mRNA,
 complete cds

Seq. No. 401677
 Seq. ID LIB3431-045-P1-N1-D10
 Method BLASTX
 NCBI GI g1835731
 BLAST score 359
 E value 4.0e-34
 Match length 80
 % identity 88
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 401678
 Seq. ID LIB3431-045-P1-N1-D11
 Method BLASTN
 NCBI GI g1815627
 BLAST score 137
 E value 7.0e-71
 Match length 137
 % identity 100
 NCBI Description Oryza sativa metallothionein-like type 2 (OsMT-2) mRNA,

Seq. ID LIB3431-045-P1-N1-G2
Method BLASTX
NCBI GI g167097
BLAST score 151
E value 7.0e-15
Match length 47
% identity 91
NCBI Description (M55449) ribulose 1,5-bisphosphate carboxylase activase
[Hordeum vulgare]

Seq. No. 401700
Seq. ID LIB3431-045-P1-N1-G6
Method BLASTX
NCBI GI g3914005
BLAST score 328
E value 2.0e-30
Match length 73
% identity 89
NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_1816586
(U85494) LON1 protease [Zea mays]

Seq. No. 401701
Seq. ID LIB3431-045-P1-N1-G8
Method BLASTN
NCBI GI g2570514
BLAST score 206
E value 1.0e-112
Match length 326
% identity 91
NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds

Seq. No. 401702
Seq. ID LIB3431-045-P1-N1-H10
Method BLASTN
NCBI GI g3789951
BLAST score 77
E value 2.0e-35
Match length 105
% identity 93
NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor
(Cab27) mRNA, nuclear gene encoding chloroplast protein,
complete cds

Seq. No. 401703
Seq. ID LIB3431-045-P1-N1-H2
Method BLASTN
NCBI GI g4105602
BLAST score 343
E value 0.0e+00
Match length 371
% identity 98
NCBI Description Oryza sativa metallothionein (MTe) gene, complete cds

Seq. No. 401704
Seq. ID LIB3431-045-P1-N1-H3
Method BLASTN
NCBI GI g5912298

BLAST score 45
 E value 5.0e-16
 Match length 59
 % identity 95
 NCBI Description Oryza sativa mRNA for gigantea homologue, partial

Seq. No. 401705
 Seq. ID LIB3431-045-P1-N1-H4
 Method BLASTX
 NCBI GI g1172977
 BLAST score 327
 E value 2.0e-30
 Match length 69
 % identity 87
 NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No. 401706
 Seq. ID LIB3431-045-P1-N1-H6
 Method BLASTX
 NCBI GI g3036951
 BLAST score 301
 E value 2.0e-27
 Match length 58
 % identity 100
 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 401707
 Seq. ID LIB3431-046-P1-K1-A1
 Method BLASTX
 NCBI GI g1353352
 BLAST score 483
 E value 1.0e-48
 Match length 149
 % identity 57
 NCBI Description (U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No. 401708
 Seq. ID LIB3431-046-P1-K1-A10
 Method BLASTX
 NCBI GI g6006363
 BLAST score 288
 E value 7.0e-26
 Match length 58
 % identity 98
 NCBI Description (AP000559) ESTs AU078183(C62904),C73912(E21020) correspond to a region of the predicted gene.; Similar to water stress inducible protein (U74296) [Oryza sativa]

Seq. No. 401709
 Seq. ID LIB3431-046-P1-K1-A11
 Method BLASTX
 NCBI GI g4105561
 BLAST score 684
 E value 3.0e-72

Match length 139
 % identity 97
 NCBI Description (AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]

Seq. No. 401710
 Seq. ID LIB3431-046-P1-K1-A12
 Method BLASTX
 NCBI GI g115787
 BLAST score 438
 E value 3.0e-43
 Match length 106
 % identity 85
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 401711
 Seq. ID LIB3431-046-P1-K1-A3
 Method BLASTX
 NCBI GI g320618
 BLAST score 465
 E value 1.0e-46
 Match length 108
 % identity 83
 NCBI Description chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf_1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No. 401712
 Seq. ID LIB3431-046-P1-K1-A4
 Method BLASTX
 NCBI GI g2288969
 BLAST score 422
 E value 2.0e-41
 Match length 122
 % identity 70
 NCBI Description (Y12862) glutathione transferase [Zea mays]

Seq. No. 401713
 Seq. ID LIB3431-046-P1-K1-A6
 Method BLASTX
 NCBI GI g320618
 BLAST score 712
 E value 2.0e-75
 Match length 159
 % identity 86
 NCBI Description chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf_1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No. 401714

Seq. ID LIB3431-046-P1-K1-A7
 Method BLASTX
 NCBI GI g3075488
 BLAST score 545
 E value 5.0e-56
 Match length 107
 % identity 98
 NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 401715
 Seq. ID LIB3431-046-P1-K1-A8
 Method BLASTX
 NCBI GI g100454
 BLAST score 627
 E value 2.0e-65
 Match length 154
 % identity 77
 NCBI Description photosystem II oxygen-evolving complex protein 1 - potato
 >gi_809113_emb_CAA35601_ (X17578)- 33kDa precursor protein
 of oxygen-evolving complex [Solanum tuberosum]

Seq. No. 401716
 Seq. ID LIB3431-046-P1-K1-B10
 Method BLASTX
 NCBI GI g6093830
 BLAST score 155
 E value 2.0e-10
 Match length 37
 % identity 81
 NCBI Description PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME)
 [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II
 PROTEIN PSBY-2] >gi_3337435 (AF060198) PsbY precursor;
 putative photosystem II peptide [Spinacia oleracea]

Seq. No. 401717
 Seq. ID LIB3431-046-P1-K1-B11
 Method BLASTX
 NCBI GI g82080
 BLAST score 433
 E value 9.0e-43
 Match length 124
 % identity 67
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
 >gi_226872_prf_1609235A chlorophyll a/b binding protein
 [Lycopersicon esculentum]

Seq. No. 401718
 Seq. ID LIB3431-046-P1-K1-B12
 Method BLASTX
 NCBI GI g3395439
 BLAST score 266
 E value 4.0e-23
 Match length 81
 % identity 62
 NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No. 401719

BLAST score 583
E value 2.0e-60
Match length 109
% identity 98
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 401725
Seq. ID LIB3431-046-P1-K1-C4
Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 9.0e-20
Match length 44
% identity 100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 401726
Seq. ID LIB3431-046-P1-K1-C6
Method BLASTN
NCBI GI g3377792
BLAST score 76
E value 4.0e-35
Match length 95
% identity 96
NCBI Description Oryza sativa ribulose-1,5-bisphosphate carboxylase/oxygenase activase (rca) mRNA, complete cds

Seq. No. 401727
Seq. ID LIB3431-046-P1-K1-C7
Method BLASTX
NCBI GI g132105
BLAST score 632
E value 4.0e-66
Match length 137
% identity 88
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401728
Seq. ID LIB3431-046-P1-K1-C8
Method BLASTX
NCBI GI g1617197
BLAST score 293
E value 2.0e-26
Match length 76
% identity 74
NCBI Description (Z72488) CP12 [Nicotiana tabacum]

09684016-101000

Seq. ID LIB3431-046-P1-K1-D6
Method BLASTX
NCBI GI g2072555
BLAST score 175
E value 1.0e-12
Match length 32
% identity 100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
protein [Oryza sativa]

Seq. No. 401735
Seq. ID LIB3431-046-P1-K1-D8
Method BLASTX
NCBI GI g1519249
BLAST score 697
E value 1.0e-73
Match length 146
% identity 95
NCBI Description (U65956) GF14-b protein [Oryza sativa]

Seq. No. 401736
Seq. ID LIB3431-046-P1-K1-D9
Method BLASTX
NCBI GI g5738522
BLAST score 180
E value 2.0e-13
Match length 50
% identity 72
NCBI Description (AL109846) putative pre-mrna splicing factor atp-dependent
rna helicase [Schizosaccharomyces pombe]

Seq. No. 401737
Seq. ID LIB3431-046-P1-K1-E1
Method BLASTX
NCBI GI g417260
BLAST score 381
E value 1.0e-36
Match length 121
% identity 64
NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
light-regulated gene [Oryza sativa]

Seq. No. 401738
Seq. ID LIB3431-046-P1-K1-E12
Method BLASTX
NCBI GI g115787
BLAST score 540
E value 2.0e-55
Match length 123
% identity 88
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
protein 2R precursor - rice >gi_20182_emb_CAA32109_
(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
[Oryza sativa]

Seq. No. 401739
 Seq. ID LIB3431-046-P1-K1-E2
 Method BLASTX
 NCBI GI g131225
 BLAST score 607
 E value 4.0e-63
 Match length 127
 % identity 92
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 401740
 Seq. ID LIB3431-046-P1-K1-E3
 Method BLASTX
 NCBI GI g6063542
 BLAST score 681
 E value 8.0e-72
 Match length 135
 % identity 100
 NCBI Description (AP000615) EST C74302(E30840) corresponds to a region of the predicted gene.; similar to glyceraldehyde-3-phosphate dehydrogenase. (M64118) [Oryza sativa]

Seq. No. 401741
 Seq. ID LIB3431-046-P1-K1-E5
 Method BLASTX
 NCBI GI g131205
 BLAST score 178
 E value 9.0e-13
 Match length 36
 % identity 100
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII (PSI-I) >gi_72677_pir_A1RZI photosystem I protein psaI - rice chloroplast >gi_11996_emb_CAA33957_ (X15901) ORF36 [Oryza sativa] >gi_226617_prf_1603356AP photosystem I small peptide [Oryza sativa]

Seq. No. 401742
 Seq. ID LIB3431-046-P1-K1-E6
 Method BLASTX
 NCBI GI g4530126
 BLAST score 236
 E value 2.0e-19
 Match length 90
 % identity 51
 NCBI Description (AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]

Seq. No. 401743
 Seq. ID LIB3431-046-P1-K1-E7
 Method BLASTX
 NCBI GI g3334333
 BLAST score 422
 E value 1.0e-41

Match length 103
 % identity 76
 NCBI Description SUPEROXIDE DISMUTASE-2 [CU-ZN] >gi_2660798 (AF034832)
 cytosolic copper/zinc superoxide dismutase
 [Mesembryanthemum crystallinum]

Seq. No. 401744
 Seq. ID LIB3431-046-P1-K1-E8
 Method BLASTX
 NCBI GI g3789954
 BLAST score 563
 E value 4.0e-58
 Match length 120
 % identity 88
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza
 sativa]

Seq. No. 401745
 Seq. ID LIB3431-046-P1-K1-E9
 Method BLASTX
 NCBI GI g4587556
 BLAST score 284
 E value 2.0e-25
 Match length 103
 % identity 53
 NCBI Description (AC006577) Similar to gi_1653162 (p)ppGpp
 3-pyrophosphohydrolase from Synechocystis sp genome
 gb_D90911. EST gb_W43807 comes from this gene.
 [Arabidopsis thaliana]

Seq. No. 401746
 Seq. ID LIB3431-046-P1-K1-F1
 Method BLASTX
 NCBI GI g115787
 BLAST score 529
 E value 5.0e-54
 Match length 121
 % identity 88
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
 protein 2R precursor - rice >gi_20182_emb_CAA32109
 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
 [Oryza sativa]

Seq. No. 401747
 Seq. ID LIB3431-046-P1-K1-F11
 Method BLASTX
 NCBI GI g3345477
 BLAST score 707
 E value 7.0e-75
 Match length 151
 % identity 90
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 401748
 Seq. ID LIB3431-046-P1-K1-F3
 Method BLASTX

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NCBI GI      g4415940
BLAST score   249
E value      3.0e-21
Match length 103
% identity   49
NCBI Description (AC006418) hypothetical protein [Arabidopsis thaliana]

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Seq. No.      401749
Seq. ID      LIB3431-046-P1-K1-F4
Method       BLASTX
NCBI GI      g82080
BLAST score   412
E value      3.0e-40
Match length  117
% identity    68
NCBI Description  chlorophyll a/b-binding protein type III precursor - tomato
                  >gi_226872_prf_1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
```

```
Seq. No.      401750
Seq. ID      LIB3431-046-P1-K1-F5
Method       BLASTX
NCBI GI      g1835731
BLAST score   507
E value      2.0e-51
Match length  123
% identity    81
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
```

Seq. No.	401751
Seq. ID	LIB3431-046-P1-K1-F6
Method	BLASTX
NCBI GI	g4512125
BLAST score	178
E value	6.0e-13
Match length	32
% identity	100
NCBI Description	(AF133340) putative chlorophyll a/b-binding protein [Phalaenopsis sp. 'KCbutterfly']

```
Seq. No.          401752
Seq. ID           LIB3431-046-P1-K1-F8
Method            BLASTX
NCBI GI           g3914603
BLAST score       680
E value           1.0e-71
Match length      131
% identity        99
NCBI Description   RIBULOSE BIPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414
                  (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase [Oryza sativa]
```

Seq. No.	401753
Seq. ID	LIB3431-046-P1-K1-G1
Method	BLASTX
NCBI GI	q3789952

```
BLAST score      612
E value         1.0e-63
Match length    121
% identity      93
NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza
sativa]
```

```

Seq. No.      401754
Seq. ID       LIB3431-046-P1-K1-G10
Method        BLASTX
NCBI GI       g132105
BLAST score    660
E value       2.0e-69
Match length  141
% identity    89
NCBI Description  RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]

```

```
Seq. No.      401755
Seq. ID      LIB3431-046-P1-K1-G11
Method       BLASTX
NCBI GI      g3914470
BLAST score   311
E value      6.0e-37
Match length  115
% identity    71
NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                >gi_1321868_emb_CAA66373_ (X97771) 10kD PSII protein
                [Hordeum vulgare]
```

```
Seq. No.      401756
Seq. ID      LIB3431-046-P1-K1-G12
Method       BLASTX
NCBI GI      g82080
BLAST score   438
E value      2.0e-44
Match length  138
% identity    68
NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
                  >gi_226872_prf_1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
```

Seq. No.	401757
Seq. ID	LIB3431-046-P1-K1-G3
Method	BLASTX
NCBI GI	g131388
BLAST score	352
E value	3.0e-33
Match length	120
% identity	65


```
Seq. ID      LIB3431-046-P1-K1-H10
Method       BLASTX
NCBI GI      g3345477
BLAST score  564
E value      5.0e-58
Match length 106
% identity   100
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
```

```
Seq. No.          401763
Seq. ID           LIB3431-046-P1-K1-H2
Method            BLASTX
NCBI GI           g2072555
BLAST score       237
E value           9.0e-20
Match length      44
% identity         100
NCBI Description   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
```

```
Seq. No.      401764
Seq. ID      LIB3431-046-P1-K1-H3
Method       BLASTX
NCBI GI      g399213
BLAST score   781
E value      2.0e-83
Match length  170
% identity    91
NCBI Description  ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG
CD4B PRECURSOR >gi_100190_pir_B35905 CD4B protein - tomato
>gi_170435 (M32604) ATP-dependent protease (CD4B)
[Lycopersicon esculentum]
```

```
Seq. No.      401765
Seq. ID      LIB3431-046-P1-K1-H4
Method       BLASTX
NCBI GI      g4079798
BLAST score   408
E value      8.0e-40
Match length  112
% identity    72
NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza
sativa]
```

```
Seq. No.          401766
Seq. ID           LIB3431-046-P1-K1-H6
Method            BLASTX
NCBI GI           g118170
BLAST score       429
E value           4.0e-42
Match length      102
% identity        85
NCBI Description   CYSTEINE PROTEINASE INHIBITOR-I (ORYZACYSTATIN-I)
                  >gi_82491_pir_A28464 oryzacystatin - rice >gi_169784
                  (J03469) oryzacystatin [Oryza sativa] >gi_169807 (M29259)
                  oryzastatin [Oryza sativa] >qi_259137 bbs_120195 (S49967)
```



```
Seq. ID      LIB3431-046-P1-N1-A11
Method       BLASTN
NCBI GI      g4105560
BLAST score  101
E value      2.0e-49
Match length 164
% identity   90
NCBI Description Oryza sativa ribulose-5-phosphate-3-epimerase (RPE) mRNA,
               complete cds
```

```
Seq. No.          401772
Seq. ID           LIB3431-046-P1-N1-A4
Method            BLASTX
NCBI GI           g2288969
BLAST score       205
E value           5.0e-16
Match length      68
% identity        54
NCBI Description  (Y12862) glutathione transferase [Zea mays]
```

```
Seq. No.          401773
Seq. ID           LIB3431-046-P1-N1-A6
Method            BLASTX
NCBI GI           g115787
BLAST score       409
E value           6.0e-40
Match length      77
% identity        100
NCBI Description  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
```

```
Seq. No.      401774
Seq. ID      LIB3431-046-P1-N1-A7
Method       BLASTX
NCBI GI      g2326947
BLAST score   224
E value      3.0e-18
Match length  44
% identity    98
NCBI Description (Z50801) Chlorophyll a/b-binding protein CP29 precursor
               [Zea mays]
```

```
Seq. No.          401775
Seq. ID           LIB3431-046-P1-N1-A8
Method            BLASTX
NCBI GI           g482311
BLAST score       244
E value           9.0e-21
Match length      50
% identity        96
NCBI Description   photosystem II oxygen-evolving complex protein 1 - rice
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                   complex protein 1 [Oryza sativa]
```


NCBI Description Sorghum bicolor BAC clone 25.M18, complete sequence

Seq. No. 401812
 Seq. ID LIB3431-046-P1-N1-H10
 Method BLASTN
 NCBI GI g606816
 BLAST score 184
 E value 3.0e-99
 Match length 208
 % identity 97
 NCBI Description Oryza sativa chloroplast carbonic anhydrase mRNA, complete cds

Seq. No. 401813
 Seq. ID LIB3431-046-P1-N1-H4
 Method BLASTN
 NCBI GI g1398998
 BLAST score 165
 E value 9.0e-88
 Match length 272
 % identity 97
 NCBI Description Rice OSOEE2 gene for 23 kDa polypeptide of photosystem II, complete cds

Seq. No. 401814
 Seq. ID LIB3431-046-P1-N1-H7
 Method BLASTX
 NCBI GI g1173347
 BLAST score 172
 E value 3.0e-12
 Match length 39
 % identity 92
 NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]

Seq. No. 401815
 Seq. ID LIB3431-046-P1-N1-H9
 Method BLASTN
 NCBI GI g2661765
 BLAST score 46
 E value 1.0e-16
 Match length 82
 % identity 89
 NCBI Description Zea mays mRNA for putative porphobilinogen deaminase

Seq. No. 401816
 Seq. ID LIB3431-047-P1-K1-A11
 Method BLASTX
 NCBI GI g482311
 BLAST score 649
 E value 4.0e-68
 Match length 129
 % identity 98

NCBI GI g132105
 BLAST score 444
 E value 4.0e-44
 Match length 104
 % identity 84
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 401827
 Seq. ID LIB3431-047-P1-K1-B2
 Method BLASTN
 NCBI GI g1732362
 BLAST score 35
 E value 4.0e-10
 Match length 43
 % identity 95
 NCBI Description Malus domestica pAFD103 mRNA, partial cds

Seq. No. 401828
 Seq. ID LIB3431-047-P1-K1-B3
 Method BLASTX
 NCBI GI g4808833
 BLAST score 311
 E value 7.0e-29
 Match length 63
 % identity 84
 NCBI Description (AF117125) endoplasmic reticulum-type calcium-transporting
 ATPase 4 [Arabidopsis thaliana]

Seq. No. 401829
 Seq. ID LIB3431-047-P1-K1-B4
 Method BLASTN
 NCBI GI g5670155
 BLAST score 42
 E value 2.0e-14
 Match length 87
 % identity 86
 NCBI Description Oryza sativa subsp. japonica BAC clone 34K24, complete
 sequence

Seq. No. 401830
 Seq. ID LIB3431-047-P1-K1-B5
 Method BLASTX
 NCBI GI g2407281
 BLAST score 641
 E value 4.0e-67
 Match length 121
 % identity 98
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
 subunit [Oryza sativa]

Seq. No. 401831
 Seq. ID LIB3431-047-P1-K1-B7
 Method BLASTX
 NCBI GI g671740
 BLAST score 354
 E value 1.0e-33
 Match length 65
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 401832
 Seq. ID LIB3431-047-P1-K1-B8
 Method BLASTX
 NCBI GI g5921799
 BLAST score 314
 E value 4.0e-29
 Match length 87
 % identity 71
 NCBI Description PUTATIVE ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT, MITOCHONDRIAL PRECURSOR (ENDOPEPTIDASE CLP)
 >gi_3559935_emb_CAA06443_ (AJ005253) ClpP protease [Mus musculus] >gi_4454289_emb_CAA09966_ (AJ012249) ClpP protease [Mus musculus]

Seq. No. 401833
 Seq. ID LIB3431-047-P1-K1-B9
 Method BLASTN
 NCBI GI g3885887
 BLAST score 41
 E value 3.0e-14
 Match length 45
 % identity 98
 NCBI Description Oryza sativa high mobility group protein (HMG) mRNA, complete cds

Seq. No. 401834
 Seq. ID LIB3431-047-P1-K1-C10
 Method BLASTN
 NCBI GI g5714761
 BLAST score 54
 E value 2.0e-21
 Match length 78
 % identity 92
 NCBI Description Oryza sativa subsp. indica serine/threonine protein phosphatase PP2A-4 catalytic subunit (PP2A) gene, complete cds

Seq. No. 401835
 Seq. ID LIB3431-047-P1-K1-C11
 Method BLASTX
 NCBI GI g3478700
 BLAST score 152
 E value 4.0e-10
 Match length 41
 % identity 66

E value	0.0e+00
Match length	369
% identity	98
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

```

Seq. No.          401846
Seq. ID           LIB3431-047-P1-K1-D3
Method            BLASTX
NCBI GI           g132105
BLAST score       532
E value           2.0e-54
Match length      122
% identity        83
NCBI Description  RIBULOSE BISPHTOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]

```

```
Seq. No.          401847
Seq. ID           LIB3431-047-P1-K1-D4
Method            BLASTX
NCBI GI           g534982
BLAST score       264
E value           5.0e-37
Match length      126
% identity        56
NCBI Description   (X75898) phosphoglucomutase [Spinacia oleracea]
```

```
Seq. No.      401848
Seq. ID      LIB3431-047-P1-K1-D7
Method       BLASTX
NCBI GI      g729478
BLAST score   476
E value      7.0e-48
Match length  102
% identity    85
NCBI Description  FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
>gi_442481 dbj_BAA04616_ (D17790) ferredoxin-NADP+
reductase [Oryza sativa] >gi_6069649 dbj_BAA85425.1_
(AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to
a region of the predicted gene.; similar to
ferredoxin-NADP+ reductase (D17790) [Oryza sativa]
```

Seq. No.	401849
Seq. ID	LIB3431-047-P1-K1-E1
Method	BLASTX
NCBI GI	g115787
BLAST score	349
E value	4.0e-33
Match length	86
% identity	84

Seq. No. 401865
 Seq. ID LIB3431-047-P1-K1-F9
 Method BLASTX
 NCBI GI g115787
 BLAST score 504
 E value 4.0e-51
 Match length 118
 % identity 86
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 401866
 Seq. ID LIB3431-047-P1-K1-G11
 Method BLASTX
 NCBI GI g132105
 BLAST score 470
 E value 3.0e-47
 Match length 107
 % identity 85
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401867
 Seq. ID LIB3431-047-P1-K1-G12
 Method BLASTX
 NCBI GI g3345477
 BLAST score 315
 E value 5.0e-29
 Match length 109
 % identity 59
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 401868
 Seq. ID LIB3431-047-P1-K1-G2
 Method BLASTX
 NCBI GI g115771
 BLAST score 864
 E value 3.0e-93
 Match length 170
 % identity 95
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi_82682_pir_S04453 chlorophyll a/b-binding protein precursor - maize >gi_22224_emb_CAA32900 (X14794) chlorophyll a/b-binding preprotein (AA 1 - 262) [Zea mays]

Seq. No. 401869

Seq. ID	LIB3431-047-P1-K1-G4
Method	BLASTX
NCBI GI	g4204276
BLAST score	421
E value	1.0e-41
Match length	107
% identity	75
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	401870
Seq. ID	LIB3431-047-P1-K1-G5
Method	BLASTX
NCBI GI	g2570511
BLAST score	506
E value	2.0e-51
Match length	105
% identity	99
NCBI Description	(AF022738) chlorophyll a-b binding protein [Oryza sativa]
Seq. No.	401871
Seq. ID	LIB3431-047-P1-K1-G6
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	2.0e-10
Match length	35
% identity	100
NCBI Description	Homo sapiens PEX1 mRNA, complete cds
Seq. No.	401872
Seq. ID	LIB3431-047-P1-K1-G7
Method	BLASTX
NCBI GI	g3126854
BLAST score	478
E value	3.0e-48
Match length	90
% identity	99
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.	401873
Seq. ID	LIB3431-047-P1-K1-G8
Method	BLASTX
NCBI GI	g3126854
BLAST score	306
E value	7.0e-48
Match length	119
% identity	85
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.	401874
Seq. ID	LIB3431-047-P1-K1-G9
Method	BLASTX
NCBI GI	g224293
BLAST score	406
E value	1.0e-39
Match length	82
% identity	99

>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 401890
 Seq. ID LIB3431-047-P1-N1-A9
 Method BLASTN
 NCBI GI g20369
 BLAST score 291
 E value 1.0e-163
 Match length 326
 % identity 98
 NCBI Description Oryza sativa shoot GS2 mRNA for chloroplastic glutamine synthetase (EC 6.3.1.2) (clone lambda-GS31)
 >gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of chloroplast localising glutamine synthetase

Seq. No. 401891
 Seq. ID LIB3431-047-P1-N1-B1
 Method BLASTN
 NCBI GI g2072554
 BLAST score 386
 E value 0.0e+00
 Match length 408
 % identity 99
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 401892
 Seq. ID LIB3431-047-P1-N1-B10
 Method BLASTX
 NCBI GI g6103011
 BLAST score 451
 E value 7.0e-45
 Match length 97
 % identity 51
 NCBI Description (X84225) precursor of photosystem II subunit (22KDa) [Nicotiana tabacum]

Seq. No. 401893
 Seq. ID LIB3431-047-P1-N1-B12
 Method BLASTN
 NCBI GI g218207
 BLAST score 181
 E value 3.0e-97
 Match length 217
 % identity 96
 NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No. 401894
 Seq. ID LIB3431-047-P1-N1-B3
 Method BLASTN
 NCBI GI g2160711
 BLAST score 320
 E value 1.0e-180
 Match length 356

00684015-101000

Seq. No. 401905
 Seq. ID LIB3431-047-P1-N1-C7
 Method BLASTX
 NCBI GI g2072555
 BLAST score 230
 E value 6.0e-19
 Match length 44
 % identity 98
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 401906
 Seq. ID LIB3431-047-P1-N1-C8
 Method BLASTX
 NCBI GI g167097
 BLAST score 189
 E value 6.0e-26
 Match length 74
 % identity 82
 NCBI Description (M55449) ribulose 1,5-bisphosphate carboxylase activase
 [Hordeum vulgare]

Seq. No. 401907
 Seq. ID LIB3431-047-P1-N1-D11
 Method BLASTN
 NCBI GI g2570514
 BLAST score 312
 E value 1.0e-175
 Match length 370
 % identity 96
 NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds

Seq. No. 401908
 Seq. ID LIB3431-047-P1-N1-D2
 Method BLASTN
 NCBI GI g20181
 BLAST score 142
 E value 5.0e-74
 Match length 156
 % identity 97
 NCBI Description Rice cab2R gene for light harvesting chlorophyll
 a/b-binding protein

Seq. No. 401909
 Seq. ID LIB3431-047-P1-N1-D3
 Method BLASTX
 NCBI GI g132105
 BLAST score 360
 E value 4.0e-34
 Match length 67
 % identity 99
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone poSSS1139) - rice >gi_218208_dbj_BAA00538_

09584016 101000

51583

% identity 96
NCBI Description Rice gene for thioredoxin h, complete cds

Seq. No. 401925
Seq. ID LIB3431-047-P1-N1-F4
Method BLASTN
NCBI GI g455510
BLAST score 132
E value 7.0e-68
Match length 136
% identity 99
NCBI Description Rice mRNA for ferritin, partial sequence

Seq. No. 401926
Seq. ID LIB3431-047-P1-N1-F6
Method BLASTX
NCBI GI g4587615
BLAST score 282
E value 5.0e-25
Match length 80
% identity 66
NCBI Description (AC006951) putative acyl-CoA synthetase [Arabidopsis thaliana] >gi_4689469_gb_AAD27905.1_AC007213_3 (AC007213) putative acyl-CoA synthetase [Arabidopsis thaliana]

Seq. No. 401927
Seq. ID LIB3431-047-P1-N1-F8
Method BLASTX
NCBI GI g3789954
BLAST score 332
E value 6.0e-31
Match length 63
% identity 98
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 401928
Seq. ID LIB3431-047-P1-N1-G11
Method BLASTX
NCBI GI g132105
BLAST score 393
E value 5.0e-38
Match length 73
% identity 99
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401929
Seq. ID LIB3431-047-P1-N1-G12
Method BLASTN

NCBI GI g3345476
 BLAST score 244
 E value 1.0e-135
 Match length 307
 % identity 95
 NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds

Seq. No. 401930
 Seq. ID LIB3431-047-P1-N1-G2
 Method BLASTN
 NCBI GI g20181
 BLAST score 56
 E value 7.0e-23
 Match length 67
 % identity 96
 NCBI Description Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No. 401931
 Seq. ID LIB3431-047-P1-N1-G4
 Method BLASTX
 NCBI GI g4204276
 BLAST score 226
 E value 2.0e-18
 Match length 73
 % identity 58
 NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 401932
 Seq. ID LIB3431-047-P1-N1-G5
 Method BLASTX
 NCBI GI g4689380
 BLAST score 260
 E value 9.0e-23
 Match length 55
 % identity 91
 NCBI Description (AF139465) LHCII type III chlorophyll a/b binding protein [Vigna radiata]

Seq. No. 401933
 Seq. ID LIB3431-047-P1-N1-G7
 Method BLASTX
 NCBI GI g115802
 BLAST score 187
 E value 3.0e-14
 Match length 36
 % identity 97
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I CAB-36) (LHCP) >gi_100311_pir_S21827 chlorophyll a/b-binding protein (cab-36) - common tobacco >gi_19827_emb_CAA41188_(X58230) chlorophyll a/b binding protein [Nicotiana tabacum]

Seq. No. 401934
 Seq. ID LIB3431-047-P1-N1-G9
 Method BLASTX
 NCBI GI g122106

BLAST score 375
 E value 5.0e-36
 Match length 77
 % identity 97
 NCBI Description HISTONE H4 >gi_70771_pir_HSZM4 histone H4 - maize
 >gi_81642_pir_S06904 histone H4 - Arabidopsis thaliana
 >gi_2119028_pir_S60475 histone H4 - garden pea
 >gi_21795_emb_CAA24924_(X00043) histone H4 [Triticum
 aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis
 thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis
 thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays]
 >gi_168501 (M13370) histone H4 [Zea mays] >gi_168503
 (M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone
 H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_
 (Z79638) histone H4 homologue [Sesbania rostrata]
 >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana]
 >gi_4580385_gb_AAD24364.1 AC007184_4 (AC007184) histone H4
 [Arabidopsis thaliana] >gi_6009915_dbj_BAA85120.1_
 (AB018245) histone H4-like protein [Solanum melongena]
 >gi_225838_prf_1314298A histone H4 [Arabidopsis thaliana]

Seq. No. 401935
 Seq. ID LIB3431-047-P1-N1-H12
 Method BLASTX
 NCBI GI g1419090
 BLAST score 320
 E value 2.0e-29
 Match length 85
 % identity 72
 NCBI Description (X94968) 37kDa chloroplast inner envelope membrane
 polypeptide precursor [Nicotiana tabacum]

Seq. No. 401936
 Seq. ID LIB3431-047-P1-N1-H4
 Method BLASTN
 NCBI GI g4079797
 BLAST score 51
 E value 1.0e-19
 Match length 106
 % identity 87
 NCBI Description Oryza sativa 23 kDa polypeptide of photosystem II mRNA,
 complete cds

Seq. No. 401937
 Seq. ID LIB3431-048-P1-K1-A10
 Method BLASTX
 NCBI GI g132105
 BLAST score 149
 E value 4.0e-10
 Match length 36
 % identity 83
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)

03684016 101000

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Seq. No.      401939
Seq. ID       LIB3431-048-P1-K1-B11
Method        BLASTX
NCBI GI       g4324967
BLAST score   195
E value       2.0e-15
Match length  38
% identity    89
NCBI Description (AF114796) ADP-ribosylation factor [Glycine max]
```

Seq. No.	401941
Seq. ID	LIB3431-048-P1-K1-B2
Method	BLASTN
NCBI GI	g4959460
BLAST score	35
E value	4.0e-10
Match length	35
% identity	100
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds

51589

09684016 101000

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Seq. No.      401944
Seq. ID      LIB3431-048-P1-K1-B5
Method       BLASTN
NCBI GI      g20369
BLAST score   143
E value      7.0e-75
Match length  158
% identity    97
NCBI Description  Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
synthetase (EC 6.3.1.2) (clone lambda-GS31)
>gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of
chloroplast localising glutamine synthetase
```

```
Seq. No.          401946
Seq. ID           LIB3431-048-P1-K1-B8
Method            BLASTX
NCBI GI           g115772
BLAST score       174
E value           5.0e-13
Match length      40
% identity        93
NCBI Description   CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
                  CAB-1) (LHCP) >gi_82460_pir_S03705 chlorophyll a/b-binding
                  protein 1R precursor - rice >gi_20178_emb_CAA32108
                  (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
                  [Oryza sativa]
```

51590

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% identity      95
NCBI Description (AJ224327) aquaporin [Oryza sativa]

Seq. No.        401948
Seq. ID         LIB3431-048-P1-K1-C12
Method          BLASTX
NCBI GI         g1917019
BLAST score     252
E value         4.0e-22
Match length    51
% identity      92
NCBI Description (U92045) ribosomal protein S6 RPS6-1 [Zea mays]

Seq. No.        401949
Seq. ID         LIB3431-048-P1-K1-C2
Method          BLASTX
NCBI GI         g2583133
BLAST score     230
E value         5.0e-19
Match length    127
% identity      38
NCBI Description (AC002387) unknown protein [Arabidopsis thaliana]

Seq. No.        401950
Seq. ID         LIB3431-048-P1-K1-C4
Method          BLASTX
NCBI GI         g4678261
BLAST score     330
E value         3.0e-31
Match length    66
% identity      91
NCBI Description (AL049657) putative proteasome regulatory subunit
[Arabidopsis thaliana]

Seq. No.        401951
Seq. ID         LIB3431-048-P1-K1-C6
Method          BLASTN
NCBI GI         g1245938
BLAST score     35
E value         7.0e-11
Match length    35
% identity      100
NCBI Description rabClC-2 beta=chloride channel ClC-2G isoform [rabbits,
heart atrium, mRNA, 2998 nt]

Seq. No.        401952
Seq. ID         LIB3431-048-P1-K1-C8
Method          BLASTN
NCBI GI         g20340
BLAST score     42
E value         9.0e-15
Match length    94
% identity      86
NCBI Description Rice rbcS gene for ribulose 1,5-bisphosphate
carboxylase/oxygenase small subunit (EC 4.1.1.39)

Seq. No.        401953

```


carboxylase S [Oryza sativa]

Seq. No. 401963
 Seq. ID LIB3431-048-P1-K1-E5
 Method BLASTX
 NCBI GI g4105131
 BLAST score 139
 E value 6.0e-09
 Match length 31
 % identity 94
 NCBI Description (AF043539) ClpC protease [Spinacia oleracea]

Seq. No. 401964
 Seq. ID LIB3431-048-P1-K1-E7
 Method BLASTX
 NCBI GI g5733874
 BLAST score 351
 E value 2.0e-33
 Match length 112
 % identity 56
 NCBI Description (AC007932) F11A17.8 [Arabidopsis thaliana]

Seq. No. 401965
 Seq. ID LIB3431-048-P1-K1-F10
 Method BLASTX
 NCBI GI g671740
 BLAST score 315
 E value 1.0e-29
 Match length 68
 % identity 87
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 401966
 Seq. ID LIB3431-048-P1-K1-F4
 Method BLASTN
 NCBI GI g2306980
 BLAST score 99
 E value 1.0e-48
 Match length 112
 % identity 97
 NCBI Description Oryza sativa photosystem I antenna protein (Lhca) mRNA, complete cds

Seq. No. 401967
 Seq. ID LIB3431-048-P1-K1-F6
 Method BLASTN
 NCBI GI g21843
 BLAST score 39
 E value 1.0e-12
 Match length 76
 % identity 88
 NCBI Description Wheat PsbO mRNA for 33kDa oxygen evolving protein of photosystem II

Seq. No. 401968
 Seq. ID LIB3431-048-P1-K1-F7

Method	BLASTX
NCBI GI	g3126854
BLAST score	151
E value	4.0e-10
Match length	33
% identity	91
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.	401969
Seq. ID	LIB3431-048-P1-K1-G10
Method	BLASTX
NCBI GI	g733454
BLAST score	266
E value	2.0e-23
Match length	74
% identity	73
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]
Seq. No.	401970
Seq. ID	LIB3431-048-P1-K1-G12
Method	BLASTX
NCBI GI	g2501189
BLAST score	444
E value	2.0e-44
Match length	90
% identity	94
NCBI Description	THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR >gi_2130146_pir_S61419 thiamine biosynthetic enzyme thil-1 - maize >gi_596078 (U17350) thiamine biosynthetic enzyme [Zea mays]
Seq. No.	401971
Seq. ID	LIB3431-048-P1-K1-G4
Method	BLASTX
NCBI GI	g671740
BLAST score	416
E value	6.0e-41
Match length	75
% identity	100
NCBI Description	(X84730) ribulose-bisphosphate carboxylase [synthetic construct]
Seq. No.	401972
Seq. ID	LIB3431-048-P1-K1-G9
Method	BLASTN
NCBI GI	g218207
BLAST score	104
E value	9.0e-52
Match length	112
% identity	98
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139
Seq. No.	401973
Seq. ID	LIB3431-048-P1-K1-H1

BLAST score 257
 E value 3.0e-22
 Match length 61
 % identity 82
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_(X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 401983
 Seq. ID LIB3431-048-P1-N1-A4
 Method BLASTX
 NCBI GI g1663724
 BLAST score 357
 E value 9.0e-34
 Match length 105
 % identity 66
 NCBI Description (U50846) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]

Seq. No. 401984
 Seq. ID LIB3431-048-P1-N1-A6
 Method BLASTN
 NCBI GI g2072554
 BLAST score 63
 E value 1.0e-26
 Match length 174
 % identity 85
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 401985
 Seq. ID LIB3431-048-P1-N1-A8
 Method BLASTN
 NCBI GI g3789953
 BLAST score 184
 E value 4.0e-99
 Match length 255
 % identity 93
 NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor (Cab26) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 401986
 Seq. ID LIB3431-048-P1-N1-B11
 Method BLASTX
 NCBI GI g2293566
 BLAST score 166
 E value 2.0e-11
 Match length 30
 % identity 100
 NCBI Description (AF012896) ADP-ribosylation factor 1 [Oryza sativa]

Seq. No. 401987
 Seq. ID LIB3431-048-P1-N1-B4
 Method BLASTX
 NCBI GI g481190
 BLAST score 301
 E value 2.0e-27

Seq. No. 401998
 Seq. ID LIB3431-048-P1-N1-D3
 Method BLASTX
 NCBI GI g3256035
 BLAST score 222
 E value 5.0e-18
 Match length 81
 % identity 52
 NCBI Description (Y14274) putative serine/threonine protein kinase [Sorghum bicolor]

Seq. No. 401999
 Seq. ID LIB3431-048-P1-N1-D5
 Method BLASTX
 NCBI GI g5257277
 BLAST score 331
 E value 7.0e-31
 Match length 68
 % identity 99
 NCBI Description (AP000364) ESTs C98431(E0144),C71728(E0144) correspond to a region of the predicted gene.; Similar to Medicago sativa S-adenosyl-L-methionine. (U20736) [Oryza sativa]

Seq. No. 402000
 Seq. ID LIB3431-048-P1-N1-D8
 Method BLASTN
 NCBI GI g435648
 BLAST score 69
 E value 2.0e-30
 Match length 105
 % identity 91
 NCBI Description Rice mRNA for gamma-Tip, complete cds

Seq. No. 402001
 Seq. ID LIB3431-048-P1-N1-D9
 Method BLASTX
 NCBI GI g1651922
 BLAST score 175
 E value 2.0e-12
 Match length 60
 % identity 55
 NCBI Description (D90901) hypothetical protein [Synechocystis sp.]

Seq. No. 402002
 Seq. ID LIB3431-048-P1-N1-E10
 Method BLASTN
 NCBI GI g19565
 BLAST score 35
 E value 4.0e-10
 Match length 47
 % identity 94
 NCBI Description M.liliiflora GADPH mRNA for glycolytic
 glyceraldehyde-3-phosphate dehydrogenase

Seq. No. 402003
 Seq. ID LIB3431-048-P1-N1-E11
 Method BLASTX

Seq. No. 402017
 Seq. ID LIB3431-048-P1-N1-G2
 Method BLASTX
 NCBI GI g4105794
 BLAST score 175
 E value 2.0e-12
 Match length 47
 % identity 60
 NCBI Description (AF049928) PGP224 [Petunia x hybrida]

Seq. No. 402018
 Seq. ID LIB3431-048-P1-N1-G4
 Method BLASTN
 NCBI GI g3063523
 BLAST score 39
 E value 1.0e-12
 Match length 59
 % identity 92
 NCBI Description Oryza sativa ribulose 1,5-bisphosphate carboxylase small subunit mRNA, complete cds

Seq. No. 402019
 Seq. ID LIB3431-048-P1-N1-G8
 Method BLASTX
 NCBI GI g4757718
 BLAST score 190
 E value 4.0e-14
 Match length 53
 % identity 66
 NCBI Description actin-like 6 >gi_4001803 (AF041474) BAF53a [Homo sapiens]
 >gi_4218064_dbj_BAA74577_ (AB015907) actin-related protein
 [Homo sapiens]

Seq. No. 402020
 Seq. ID LIB3431-048-P1-N1-G9
 Method BLASTN
 NCBI GI g218207
 BLAST score 34
 E value 1.0e-09
 Match length 98
 % identity 84
 NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No. 402021
 Seq. ID LIB3431-048-P1-N1-H10
 Method BLASTX
 NCBI GI g729478
 BLAST score 171
 E value 2.0e-12
 Match length 39
 % identity 79
 NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
 >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+ reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_ (AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to

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Seq. No.	402028
Seq. ID	LIB3431-049-P1-K1-B11
Method	BLASTX
NCBI GI	g445116
BLAST score	226
E value	2.0e-28
Match length	71
% identity	92
NCBI Description	light-harvesting complex IIa protein; [Hordeum vulgare]

Seq. No.	402030
Seq. ID	LIB3431-049-P1-K1-B2
Method	BLASTN
NCBI GI	g20181
BLAST score	74
E value	7.0e-34
Match length	81
% identity	99
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

51607

Seq. No.	402032
Seq. ID	LIB3431-049-P1-K1-B5
Method	BLASTN
NCBI GI	g4079797
BLAST score	144
E value	2.0e-75
Match length	155
% identity	99
NCBI Description	Oryza sativa 23 kDa polypeptide of photosystem II mRNA, complete cds
Seq. No.	402033
Seq. ID	LIB3431-049-P1-K1-B7
Method	BLASTX
NCBI GI	g549063
BLAST score	276
E value	5.0e-37
Match length	82
% identity	99
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa]
Seq. No.	402034
Seq. ID	LIB3431-049-P1-K1-C12
Method	BLASTX
NCBI GI	g606817
BLAST score	661
E value	4.0e-81
Match length	155
% identity	99
NCBI Description	(U08404) carbonic anhydrase [Oryza sativa] >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic anhydrase 3 [Oryza sativa]
Seq. No.	402035
Seq. ID	LIB3431-049-P1-K1-C4
Method	BLASTX
NCBI GI	g1805617
BLAST score	163
E value	5.0e-20
Match length	56
% identity	96
NCBI Description	(D49704) OSH44 transcript; homeobox gene [Oryza sativa]
Seq. No.	402036
Seq. ID	LIB3431-049-P1-K1-C5
Method	BLASTN
NCBI GI	g3885885
BLAST score	191
E value	1.0e-103
Match length	226
% identity	97
NCBI Description	Oryza sativa Rieske Fe-S precursor protein (RISP) mRNA, complete cds

Seq. No. 402037
 Seq. ID LIB3431-049-P1-K1-C7
 Method BLASTN
 NCBI GI g218171
 BLAST score 83
 E value 4.0e-39
 Match length 138
 % identity 91
 NCBI Description Oryza sativa mRNA for type I light-harvesting chlorophyll
 a/b binding protein of photosystem II (LHCPII), complete
 cds

Seq. No. 402038
 Seq. ID LIB3431-049-P1-K1-C8
 Method BLASTX
 NCBI GI g2739360
 BLAST score 152
 E value 6.0e-18
 Match length 102
 % identity 51
 NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]
 >gi_3075385 (AC004484) unknown protein [Arabidopsis
 thaliana]

Seq. No. 402039
 Seq. ID LIB3431-049-P1-K1-D1
 Method BLASTN
 NCBI GI g4218534
 BLAST score 45
 E value 2.0e-16
 Match length 45
 % identity 100
 NCBI Description Triticum sp. mRNA for GRAB1 protein

Seq. No. 402040
 Seq. ID LIB3431-049-P1-K1-D10
 Method BLASTX
 NCBI GI g3789954
 BLAST score 367
 E value 4.0e-45
 Match length 100
 % identity 95
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza
 sativa]

Seq. No. 402041
 Seq. ID LIB3431-049-P1-K1-D12
 Method BLASTX
 NCBI GI g3676294
 BLAST score 151
 E value 5.0e-21
 Match length 66
 % identity 77
 NCBI Description (U96496) mitochondrial ATPase beta subunit [Nicotiana
 sylvestris]

Seq. No. 402042

Seq. ID LIB3431-049-P1-K1-D4
 Method BLASTX
 NCBI GI g3126854
 BLAST score 345
 E value 6.0e-35
 Match length 78
 % identity 97
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 402043
 Seq. ID LIB3431-049-P1-K1-E10
 Method BLASTN
 NCBI GI g3126853
 BLAST score 150
 E value 6.0e-79
 Match length 222
 % identity 93
 NCBI Description Oryza sativa chlorophyll a/b binding protein (RCABP89)
 mRNA, nuclear gene encoding chloroplast protein, complete
 cds

Seq. No. 402044
 Seq. ID LIB3431-049-P1-K1-E11
 Method BLASTN
 NCBI GI g4138289
 BLAST score 68
 E value 4.0e-30
 Match length 72
 % identity 99
 NCBI Description Oryza sativa mRNA for thioredoxin M

Seq. No. 402045
 Seq. ID LIB3431-049-P1-K1-E9
 Method BLASTN
 NCBI GI g3885891
 BLAST score 80
 E value 7.0e-37
 Match length 95
 % identity 97
 NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F)
 mRNA, complete cds

Seq. No. 402046
 Seq. ID LIB3431-049-P1-K1-F12
 Method BLASTX
 NCBI GI g3885894
 BLAST score 266
 E value 9.0e-34
 Match length 91
 % identity 86
 NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No. 402047
 Seq. ID LIB3431-049-P1-K1-F2
 Method BLASTX
 NCBI GI g2130089
 BLAST score 219

BLAST score 345
 E value 0.0e+00
 Match length 432
 % identity 94
 NCBI Description Rice OSH45 gene for OSH42, OSH44 and OSH45 transcripts,
 exon 2, 3, 4, 5, 6 and 7, complete cds

Seq. No. 402068
 Seq. ID LIB3431-049-P1-N1-C5
 Method BLASTN
 NCBI GI g3885885
 BLAST score 195
 E value 1.0e-105
 Match length 202
 % identity 100
 NCBI Description Oryza sativa Rieske Fe-S precursor protein (RISP) mRNA,
 complete cds

Seq. No. 402069
 Seq. ID LIB3431-049-P1-N1-C7
 Method BLASTX
 NCBI GI g289920
 BLAST score 284
 E value 3.0e-25
 Match length 56
 % identity 96
 NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium
 hirsutum]

Seq. No. 402070
 Seq. ID LIB3431-049-P1-N1-C8
 Method BLASTX
 NCBI GI g2739360
 BLAST score 261
 E value 1.0e-22
 Match length 111
 % identity 52
 NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]
 >gi_3075385 (AC004484) unknown protein [Arabidopsis
 thaliana]

Seq. No. 402071
 Seq. ID LIB3431-049-P1-N1-C9
 Method BLASTN
 NCBI GI g2970050
 BLAST score 38
 E value 7.0e-12
 Match length 102
 % identity 84
 NCBI Description Vigna radiata mRNA for ARG10, complete cds

Seq. No. 402072
 Seq. ID LIB3431-049-P1-N1-D1
 Method BLASTN
 NCBI GI g398603
 BLAST score 39
 E value 2.0e-12

Seq. No. 402078
 Seq. ID LIB3431-049-P1-N1-E11
 Method BLASTN
 NCBI GI g4138289
 BLAST score 163
 E value 2.0e-86
 Match length 324
 % identity 87
 NCBI Description Oryza sativa mRNA for thioredoxin M

Seq. No. 402079
 Seq. ID LIB3431-049-P1-N1-E2
 Method BLASTX
 NCBI GI g128690
 BLAST score 529
 E value 8.0e-54
 Match length 116
 % identity 90
 NCBI Description NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 3, CHLOROPLAST
 >gi_66161_pir_DERZN3 NADH dehydrogenase (ubiquinone) (EC
 1.6.5.3) chain 3 - rice chloroplast >gi_11989_emb_CAA34001_
 (X15901) ndhC; NADH dehydrogenase ND3 [Oryza sativa]
 >gi_226610_prf_1603356AG NADH dehydrogenase ND3 [Oryza
 sativa]

Seq. No. 402080
 Seq. ID LIB3431-049-P1-N1-E9
 Method BLASTX
 NCBI GI g3885892
 BLAST score 200
 E value 1.0e-15
 Match length 49
 % identity 82
 NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 402081
 Seq. ID LIB3431-049-P1-N1-F12
 Method BLASTX
 NCBI GI g3885894
 BLAST score 178
 E value 5.0e-13
 Match length 59
 % identity 68
 NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No. 402082
 Seq. ID LIB3431-049-P1-N1-F2
 Method BLASTX
 NCBI GI g2130089
 BLAST score 439
 E value 2.0e-43
 Match length 88
 % identity 90
 NCBI Description 2-oxoglutarate/malate translocator (clone OMT103),
 mitochondrial membrane - proso millet
 >gi_1100743_dbj_BAA08105_ (D45075) 2-oxoglutarate/malate
 translocator [Panicum miliaceum]

Seq. ID	LIB3431-049-P1-N1-G3
Method	BLASTN
NCBI GI	g3885891
BLAST score	34
E value	5.0e-10
Match length	58
% identity	90
NCBI Description	Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds
Seq. No.	402089
Seq. ID	LIB3431-049-P1-N1-G6
Method	BLASTX
NCBI GI	g6006283
BLAST score	162
E value	3.0e-11
Match length	41
% identity	71
NCBI Description	(AB015861) photosystem I subunit PSI-L [Arabidopsis thaliana]
Seq. No.	402090
Seq. ID	LIB3431-049-P1-N1-G7
Method	BLASTX
NCBI GI	g551047
BLAST score	243
E value	2.0e-20
Match length	55
% identity	85
NCBI Description	(X79277) type II LHCI [Lolium temulentum]
Seq. No.	402091
Seq. ID	LIB3431-049-P1-N1-G8
Method	BLASTN
NCBI GI	g218207
BLAST score	180
E value	1.0e-96
Match length	279
% identity	90
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139
Seq. No.	402092
Seq. ID	LIB3431-049-P1-N1-H5
Method	BLASTX
NCBI GI	g4262142
BLAST score	145
E value	5.0e-09
Match length	69
% identity	49
NCBI Description	(AC005275) putative alcohol dehydrogenase [Arabidopsis thaliana]
Seq. No.	402093
Seq. ID	LIB3431-049-P1-N1-H6
Method	BLASTX

NCBI GI g671740
 BLAST score 380
 E value 2.0e-36
 Match length 69
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 402094
 Seq. ID LIB3431-049-P1-N1-H7
 Method BLASTX
 NCBI GI g21839
 BLAST score 336
 E value 2.0e-31
 Match length 75
 % identity 87
 NCBI Description (X57952) phosphoribulokinase [Triticum aestivum]

Seq. No. 402095
 Seq. ID LIB3431-050-P1-K1-A10
 Method BLASTN
 NCBI GI g2062705
 BLAST score 35
 E value 5.0e-10
 Match length 35
 % identity 100
 NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 402096
 Seq. ID LIB3431-050-P1-K1-A11
 Method BLASTX
 NCBI GI g131192
 BLAST score 449
 E value 1.0e-44
 Match length 97
 % identity 87
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR
 (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi_100606_pir__S20937
 photosystem I chain V precursor - barley
 >gi_19091_emb_CAA42727_ (X60158) photosystem I polypeptide
 PSI-G precursor [Hordeum vulgare]

Seq. No. 402097
 Seq. ID LIB3431-050-P1-K1-A2
 Method BLASTX
 NCBI GI g132105
 BLAST score 339
 E value 4.0e-32
 Match length 79
 % identity 86
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

09684016.101000

% identity 97
NCBI Description Oryza sativa mRNA for the small subunit of
ribulose-1,5-bisphosphate carboxylase, complete cds, clone
pOSSS1139

Seq. No. 402103
Seq. ID LIB3431-050-P1-K1-B10
Method BLASTN
NCBI GI g20262
BLAST score 268
E value 1.0e-149
Match length 308
% identity 97
NCBI Description O.sativa light-induced mRNA

Seq. No. 402104
Seq. ID LIB3431-050-P1-K1-B2
Method BLASTX
NCBI GI g320618
BLAST score 290
E value 3.0e-26
Match length 70
% identity 79
NCBI Description chlorophyll a/b-binding protein I precursor - rice
>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
>gi_227611_prf_1707316A chlorophyll a/b binding protein 1
[Oryza sativa]

Seq. No. 402105
Seq. ID LIB3431-050-P1-K1-B3
Method BLASTX
NCBI GI g3367596
BLAST score 311
E value 6.0e-32
Match length 98
% identity 70
NCBI Description (AL031135) putative protein [Arabidopsis thaliana]

Seq. No. 402106
Seq. ID LIB3431-050-P1-K1-B7
Method BLASTX
NCBI GI g2924785
BLAST score 165
E value 2.0e-11
Match length 79
% identity 47
NCBI Description (AC002334) similar to disease resistance protein
[Arabidopsis thaliana]

Seq. No. 402107
Seq. ID LIB3431-050-P1-K1-C1
Method BLASTX
NCBI GI g3236242
BLAST score 435
E value 4.0e-43
Match length 106

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% identity      80
NCBI Description (AC004684) putative ribosomal protein L36 [Arabidopsis
                  thaliana]

Seq. No.        402108
Seq. ID         LIB3431-050-P1-K1-C12
Method          BLASTX
NCBI GI         g82080
BLAST score     364
E value         8.0e-35
Match length    103
% identity      70
NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
                  >gi_226872_prf_1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]

Seq. No.        402109
Seq. ID         LIB3431-050-P1-K1-C2
Method          BLASTX
NCBI GI         g3036953
BLAST score     273
E value         5.0e-24
Match length    51
% identity      100
NCBI Description (AB012640) light harvesting chlorophyll a/b-binding protein
                  [Nicotiana sylvestris]

Seq. No.        402110
Seq. ID         LIB3431-050-P1-K1-C7
Method          BLASTX
NCBI GI         g3808101
BLAST score     335
E value         2.0e-33
Match length    99
% identity      70
NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]

Seq. No.        402111
Seq. ID         LIB3431-050-P1-K1-C9
Method          BLASTX
NCBI GI         g132105
BLAST score     480
E value         2.0e-48
Match length    112
% identity      82
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]

Seq. No.        402112
Seq. ID         LIB3431-050-P1-K1-D1
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Method BLASTX
NCBI GI g3929924
BLAST score 210
E value 4.0e-17
Match length 41
% identity 100
NCBI Description (AB020502) catalase [Oryza sativa]

Seq. No. 402113
Seq. ID LIB3431-050-P1-K1-D10
Method BLASTX
NCBI GI g462195
BLAST score 281
E value 5.0e-25
Match length 69
% identity 81
NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
>gi_100682_pir_S21636 GOS2 protein - rice
>gi_20238_emb_CAA36190 (X51910) GOS2 [Oryza sativa]
>gi_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No. 402114
Seq. ID LIB3431-050-P1-K1-D11
Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 7.0e-20
Match length 44
% identity 100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 402115
Seq. ID LIB3431-050-P1-K1-D2
Method BLASTN
NCBI GI g6015437
BLAST score 36
E value 8.0e-11
Match length 36
% identity 100
NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 402116
Seq. ID LIB3431-050-P1-K1-D3
Method BLASTX
NCBI GI g1370188
BLAST score 304
E value 5.0e-28
Match length 71
% identity 79
NCBI Description (Z73943) RAB7D [Lotus japonicus]

Seq. No. 402117
Seq. ID LIB3431-050-P1-K1-D6
Method BLASTX

NCBI Description (AB004871) CPC [Arabidopsis thaliana]
>gi_4559383_gb_AAD23043.1_AC006526_8 (AC006526) putative
DNA binding protein CPC [Arabidopsis thaliana]

Seq. No. 402123
Seq. ID LIB3431-050-P1-K1-E4
Method BLASTX
NCBI GI g3915186
BLAST score 231
E value 4.0e-19
Match length 86
% identity 55
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-21 KD (UBIQUITIN-PROTEIN
LIGASE) (UBIQUITIN CARRIER PROTEIN) (PEROXIN-4) >gi_3128447
(AF061604) ubiquitin-conjugating enzyme homolog peroxin 4
[Pichia angusta]

Seq. No. 402124
Seq. ID LIB3431-050-P1-K1-E7
Method BLASTN
NCBI GI g6015437
BLAST score 36
E value 9.0e-11
Match length 36
% identity 100
NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 402125
Seq. ID LIB3431-050-P1-K1-E9
Method BLASTX
NCBI GI g3036946
BLAST score 281
E value 3.0e-25
Match length 56
% identity 95
NCBI Description (AB012637) light harvesting chlorophyll a/b-binding protein
[Nicotiana glauca]

Seq. No. 402126
Seq. ID LIB3431-050-P1-K1-F1
Method BLASTX
NCBI GI g125580
BLAST score 155
E value 8.0e-11
Match length 48
% identity 73
NCBI Description PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
(PRK) >gi_100839_pir_S15743 phosphoribulokinase (EC
2.7.1.19) - wheat >gi_5924030_emb_CAB56544.1_ (X51608)
phosphoribulokinase [Triticum aestivum]

Seq. No. 402127
Seq. ID LIB3431-050-P1-K1-F11
Method BLASTX
NCBI GI g4572679
BLAST score 161
E value 2.0e-11

E value	2.0e-50
Match length	102
% identity	96
NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

```
Seq. No.          402133
Seq. ID           LIB3431-050-P1-K1-G1
Method            BLASTN
NCBI GI           g6006355
BLAST score       125
E value           8.0e-64
Match length      260
% identity        100
NCBI Description   Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
```

```
Seq. No.      402134
Seq. ID       LIB3431-050-P1-K1-G10
Method        BLASTX
NCBI GI       g4680501
BLAST score    216
E value       2.0e-17
Match length   91
% identity     52
NCBI Description (AF119222) hypothetical protein [Oryza sativa]
```

```
Seq. No.          402135
Seq. ID           LIB3431-050-P1-K1-G11
Method            BLASTX
NCBI GI           g21693
BLAST score       450
E value           5.0e-45
Match length      83
% identity        92
NCBI Description   (X66012) cathepsin B [Triticum aestivum]
```

```
Seq. No.      402136
Seq. ID      LIB3431-050-P1-K1-G4
Method       BLASTN
NCBI GI      g4959460
BLAST score   38
E value      9.0e-12
Match length  38
% identity    100
NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds
```

```
Seq. No.          402137
Seq. ID           LIB3431-050-P1-K1-G5
Method            BLASTX
NCBI GI           g3687440
BLAST score       310
E value           1.0e-28
Match length      107
% identity        54
NCBI Description   (AL022577) dJ353H6.2.1 (SW1/SNF related, matrix associated,
                  actin dependent regulator of chromatin, subfamily a, member
                  1 (SNF2L1)) [Homo sapiens]
```

Seq. No. 402138
 Seq. ID LIB3431-050-P1-K1-G7
 Method BLASTX
 NCBI GI g417260
 BLAST score 349
 E value 5.0e-33
 Match length 110
 % identity 66
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

Seq. No. 402139
 Seq. ID LIB3431-050-P1-K1-G8
 Method BLASTX
 NCBI GI g1944407
 BLAST score 265
 E value 3.0e-23
 Match length 65
 % identity 72
 NCBI Description (D86988) KIAA0221 [Homo sapiens]

Seq. No. 402140
 Seq. ID LIB3431-050-P1-K1-H11
 Method BLASTX
 NCBI GI g2072555
 BLAST score 233
 E value 2.0e-19
 Match length 44
 % identity 98
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 402141
 Seq. ID LIB3431-050-P1-K1-H2
 Method BLASTX
 NCBI GI g320618
 BLAST score 406
 E value 9.0e-40
 Match length 96
 % identity 80
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 402142
 Seq. ID LIB3431-050-P1-K1-H3
 Method BLASTX
 NCBI GI g430947
 BLAST score 390
 E value 6.0e-38
 Match length 104
 % identity 72

NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein
[Arabidopsis thaliana]

Seq. No. 402143
Seq. ID LIB3431-050-P1-K1-H4
Method BLASTX
NCBI GI g132105
BLAST score 251
E value 8.0e-22
Match length 67
% identity 76

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 402144
Seq. ID LIB3431-050-P1-K1-H5
Method BLASTX
NCBI GI g2570515
BLAST score 488
E value 3.0e-49
Match length 110
% identity 86
NCBI Description (AF022740) glycolate oxidase [Oryza sativa]

Seq. No. 402145
Seq. ID LIB3431-050-P1-K1-H9
Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 7.0e-20
Match length 44
% identity 100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
protein [Oryza sativa]

Seq. No. 402146
Seq. ID LIB3431-050-P1-N1-A11
Method BLASTX
NCBI GI g131192
BLAST score 359
E value 3.0e-34
Match length 74
% identity 89
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR
(PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi_100606_pir_S20937
photosystem I chain V precursor - barley
>gi_19091_emb_CAA42727_ (X60158) photosystem I polypeptide
PSI-G precursor [Hordeum vulgare]

Seq. No. 402147
 Seq. ID LIB3431-050-P1-N1-A2
 Method BLASTX
 NCBI GI g347451
 BLAST score 291
 E value 4.0e-26
 Match length 57
 % identity 98
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 402148
 Seq. ID LIB3431-050-P1-N1-A6
 Method BLASTX
 NCBI GI g2072555
 BLAST score 279
 E value 1.0e-24
 Match length 54
 % identity 93
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 402149
 Seq. ID LIB3431-050-P1-N1-A9
 Method BLASTX
 NCBI GI g2499417
 BLAST score 277
 E value 1.0e-24
 Match length 62
 % identity 82
 NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
 >gi_1085826_pir_S49248 H-protein - Flaveria anomala
 >gi_547558_emb_CAA85761_ (Z37524) H-protein [Flaveria anomala]

Seq. No. 402150
 Seq. ID LIB3431-050-P1-N1-B10
 Method BLASTN
 NCBI GI g20262
 BLAST score 146
 E value 2.0e-76
 Match length 274
 % identity 89
 NCBI Description O.sativa light-induced mRNA

Seq. No. 402151
 Seq. ID LIB3431-050-P1-N1-B11
 Method BLASTX
 NCBI GI g4587570
 BLAST score 144
 E value 8.0e-09
 Match length 66
 % identity 45
 NCBI Description (AC006550) Strong similarity to gi_2244833 centromere protein homolog from Arabidopsis thaliana chromosome 4 contig gb_Z97337. ESTs gb_T20765 and gb_AA586277 come from

this gene

Seq. No. 402152
Seq. ID LIB3431-050-P1-N1-B2
Method BLASTX
NCBI GI g115787
BLAST score 480
E value 3.0e-48
Match length 92
% identity 99
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2' PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 402153
Seq. ID LIB3431-050-P1-N1-B5
Method BLASTX
NCBI GI g1429226
BLAST score 228
E value 1.0e-18
Match length 47
% identity 85
NCBI Description (X98861) TFIIA [Arabidopsis thaliana]

Seq. No. 402154
Seq. ID LIB3431-050-P1-N1-B8
Method BLASTX
NCBI GI g5729802
BLAST score 452
E value 6.0e-45
Match length 91
% identity 89
NCBI Description similar to S. pombe dim1+ >gi_2565275 (AF023611) Dimlp homolog [Homo sapiens]

Seq. No. 402155
Seq. ID LIB3431-050-P1-N1-C1
Method BLASTX
NCBI GI g3236242
BLAST score 334
E value 4.0e-31
Match length 98
% identity 69
NCBI Description (AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]

Seq. No. 402156
Seq. ID LIB3431-050-P1-N1-C11
Method BLASTX
NCBI GI g131176
BLAST score 203
E value 6.0e-16
Match length 47
% identity 87
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR

BLAST score 150
E value 8.0e-79
Match length 250
% identity 91
NCBI Description Oryza sativa CatC gene for catalase, complete cds

Seq. No. 402162
Seq. ID LIB3431-050-P1-N1-D10
Method BLASTN
NCBI GI g3789949
BLAST score 186
E value 1.0e-100
Match length 298
% identity 91
NCBI Description Oryza sativa translation initiation factor (GOS2) mRNA, complete cds

Seq. No. 402163
Seq. ID LIB3431-050-P1-N1-D11
Method BLASTX
NCBI GI g2072555
BLAST score 333
E value 5.0e-31
Match length 62
% identity 97
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 402164
Seq. ID LIB3431-050-P1-N1-D4
Method BLASTX
NCBI GI g4680212
BLAST score 187
E value 7.0e-14
Match length 53
% identity 66
NCBI Description (AF114171) hypothetical protein [Sorghum bicolor]

Seq. No. 402165
Seq. ID LIB3431-050-P1-N1-D7
Method BLASTX
NCBI GI g5541681
BLAST score 212
E value 7.0e-17
Match length 92
% identity 55
NCBI Description (AL096859) putative protein [Arabidopsis thaliana]

Seq. No. 402166
Seq. ID LIB3431-050-P1-N1-E1
Method BLASTX
NCBI GI g1835731
BLAST score 187
E value 1.0e-28
Match length 88
% identity 80

NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 402167
Seq. ID LIB3431-050-P1-N1-E5
Method BLASTN
NCBI GI g11957
BLAST score 323
E value 0.0e+00
Match length 431
% identity 99
NCBI Description Rice complete chloroplast genome

Seq. No. 402168
Seq. ID LIB3431-050-P1-N1-E9
Method BLASTN
NCBI GI g20181
BLAST score 43
E value 6.0e-15
Match length 146
% identity 82
NCBI Description Rice cab2R gene for light harvesting chlorophyll
a/b-binding protein

Seq. No. 402169
Seq. ID LIB3431-050-P1-N1-F1
Method BLASTX
NCBI GI g21839
BLAST score 340
E value 8.0e-32
Match length 73
% identity 93
NCBI Description (X57952) phosphoribulokinase [Triticum aestivum]

Seq. No. 402170
Seq. ID LIB3431-050-P1-N1-F12
Method BLASTN
NCBI GI g3273244
BLAST score 46
E value 1.0e-16
Match length 62
% identity 94
NCBI Description Oryza sativa DNA for NLS receptor, complete cds

Seq. No. 402171
Seq. ID LIB3431-050-P1-N1-F3
Method BLASTX
NCBI GI g1172555
BLAST score 184
E value 2.0e-13
Match length 61
% identity 57
NCBI Description 34 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN
(VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
(POM 34) >gi_629720_pir_S46936 34K porin - potato
>gi_1076682_pir_A55364 porin (clone pPOM-34) - potato
mitochondrion >gi_516166_emb_CAA56599_ (X80386) 34 kDa
porin [Solanum tuberosum]

BLAST score 38
 E value 5.0e-12
 Match length 42
 % identity 98
 NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds

Seq. No. 402178
 Seq. ID LIB3431-050-P1-N1-H2
 Method BLASTX
 NCBI GI g421916
 BLAST score 168
 E value 1.0e-11
 Match length 31
 % identity 100
 NCBI Description chlorophyll a/b-binding protein - English ivy (fragment)
 >gi_12582_emb_CAA48410_ (X68333) light harvesting
 chlorophyll a/b binding protein [Hedera helix]

Seq. No. 402179
 Seq. ID LIB3431-050-P1-N1-H4
 Method BLASTN
 NCBI GI g218207
 BLAST score 72
 E value 3.0e-32
 Match length 174
 % identity 85
 NCBI Description Oryza sativa mRNA for the small subunit of
 ribulose-1,5-bisphosphate carboxylase, complete cds, clone
 pOSSS1139

Seq. No. 402180
 Seq. ID LIB3431-050-P1-N1-H5
 Method BLASTN
 NCBI GI g2570514
 BLAST score 240
 E value 1.0e-132
 Match length 335
 % identity 93
 NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds

Seq. No. 402181
 Seq. ID LIB3431-050-P1-N1-H9
 Method BLASTN
 NCBI GI g2072554
 BLAST score 135
 E value 6.0e-70
 Match length 183
 % identity 93
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
 cds

Seq. No. 402182
 Seq. ID LIB3431-051-P1-K1-A11
 Method BLASTX
 NCBI GI g2072555
 BLAST score 313
 E value 8.0e-29

Match length 62
 % identity 90
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 402183
 Seq. ID LIB3431-051-P1-K1-A3
 Method BLASTN
 NCBI GI g20177
 BLAST score 102
 E value 2.0e-50
 Match length 123
 % identity 98
 NCBI Description Rice cab1R gene for light harvesting chlorophyll
 a/b-binding protein

Seq. No. 402184
 Seq. ID LIB3431-051-P1-K1-A5
 Method BLASTX
 NCBI GI g5103807
 BLAST score 349
 E value 5.0e-33
 Match length 93
 % identity 69
 NCBI Description (AC007591) Contains similarity to gb_AF014403 type-2
 phosphatidic acid phosphatase alpha-2 (PAP2_a2) from Homo
 sapiens. ESTs gb_T88254 and gb_AA394650 come from this
 gene. [Arabidopsis thaliana]

Seq. No. 402185
 Seq. ID LIB3431-051-P1-K1-A6
 Method BLASTN
 NCBI GI g5456937
 BLAST score 54
 E value 1.0e-21
 Match length 54
 % identity 100
 NCBI Description Oryza sativa rps9 mRNA for ribosomal protein S9, complete
 cds

Seq. No. 402186
 Seq. ID LIB3431-051-P1-K1-A9
 Method BLASTX
 NCBI GI g3885886
 BLAST score 642
 E value 2.0e-67
 Match length 125
 % identity 100
 NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]

Seq. No. 402187
 Seq. ID LIB3431-051-P1-K1-B1
 Method BLASTX
 NCBI GI g3913018
 BLAST score 494
 E value 5.0e-50

Match length 101
 % identity 99
 NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
 (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic
 aldolase [Oryza sativa]

Seq. No. 402188
 Seq. ID LIB3431-051-P1-K1-B12
 Method BLASTX
 NCBI GI g733454
 BLAST score 450
 E value 8.0e-45
 Match length 108
 % identity 80
 NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
 [Zea mays]

Seq. No. 402189
 Seq. ID LIB3431-051-P1-K1-B2
 Method BLASTX
 NCBI GI g2407281
 BLAST score 517
 E value 1.0e-52
 Match length 107
 % identity 93
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
 subunit [Oryza sativa]

Seq. No. 402190
 Seq. ID LIB3431-051-P1-K1-B3
 Method BLASTX
 NCBI GI g3126854
 BLAST score 534
 E value 8.0e-55
 Match length 102
 % identity 96
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 402191
 Seq. ID LIB3431-051-P1-K1-B6
 Method BLASTX
 NCBI GI g606817
 BLAST score 489
 E value 2.0e-49
 Match length 93
 % identity 99
 NCBI Description (U08404) carbonic anhydrase [Oryza sativa]
 >gi_5917783_gb_AAD56038.1 AF182806_1 (AF182806) carbonic
 anhydrase 3 [Oryza sativa]

Seq. No. 402192
 Seq. ID LIB3431-051-P1-K1-B7
 Method BLASTN
 NCBI GI g2624327
 BLAST score 141
 E value 2.0e-73
 Match length 201

% identity 93
 NCBI Description Oryza sativa mRNA for glycine rich RNA-binding protein 2 (OsGRP2)

Seq. No. 402193
 Seq. ID LIB3431-051-P1-K1-B8
 Method BLASTX
 NCBI GI g2499932
 BLAST score 479
 E value 2.0e-48
 Match length 105
 % identity 87
 NCBI Description ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi_726305 (U22442) adenine phosphoribosyltransferase form 1 [Triticum aestivum]

Seq. No. 402194
 Seq. ID LIB3431-051-P1-K1-C1
 Method BLASTX
 NCBI GI g2982453
 BLAST score 474
 E value 9.0e-48
 Match length 109
 % identity 83
 NCBI Description (AL022223) fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana]

Seq. No. 402195
 Seq. ID LIB3431-051-P1-K1-C10
 Method BLASTX
 NCBI GI g124224
 BLAST score 511
 E value 9.0e-55
 Match length 121
 % identity 90
 NCBI Description INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D) >gi_100345_pir_S21060 translation initiation factor eIF-5A - common tobacco >gi_19887_emb_CAA45105_ (X63543) eukaryotic initiation factor 5A (3) [Nicotiana tabacum]

Seq. No. 402196
 Seq. ID LIB3431-051-P1-K1-C11
 Method BLASTX
 NCBI GI g2492514
 BLAST score 525
 E value 1.0e-53
 Match length 110
 % identity 94
 NCBI Description CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR >gi_1483215_emb_CAA68141_ (X99808) chloroplast FtsH protease [Arabidopsis thaliana]

Seq. No. 402197
 Seq. ID LIB3431-051-P1-K1-C12
 Method BLASTX
 NCBI GI g115825
 BLAST score 272

NCBI GI	g304219
BLAST score	80
E value	4.0e-37
Match length	179
% identity	86
NCBI Description	Hordeum vulgare chloroplast photosystem I PSK-I subunit mRNA, complete cds

Seq. No.	402203
Seq. ID	LIB3431-051-P1-K1-D12
Method	BLASTN
NCBI GI	g5106774
BLAST score	63
E value	7.0e-27
Match length	188
% identity	84
NCBI Description	Hordeum vulgare ribosomal protein S12 (rps12) mRNA, complete cds

```
Seq. No.          402204
Seq. ID           LIB3431-051-P1-K1-D2
Method            BLASTX
NCBI GI           g4585882
BLAST score       532
E value           2.0e-54
Match length      119
% identity        80
NCBI Description   (AC005850) PSI type III chlorophyll a/b-binding protein
                  [Arabidopsis thaliana]
```

```
Seq. No.          402205
Seq. ID           LIB3431-051-P1-K1-D3
Method            BLASTN
NCBI GI           g3789951
BLAST score       111
E value           2.0e-55
Match length      252
% identity         92
NCBI Description   Oryza sativa chlorophyll a/b-binding protein presursor
                  (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
```

Seq. No.	402206
Seq. ID	LIB3431-051-P1-K1-D4
Method	BLASTN
NCBI GI	g20181
BLAST score	123
E value	1.0e-62
Match length	130
% identity	98
NCBI Description	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein

Seq. No.	402207
Seq. ID	LIB3431-051-P1-K1-D5
Method	BLASTX
NCBI GI	q132166


```

BLAST score      160
E value         6.0e-11
Match length    31
% identity      87
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
                  >gi_81660_pir_S04048 ribulose-bisphosphate carboxylase
                  activase precursor - Arabidopsis thaliana
                  >gi_16471_emb_CAA32429 (X14212) rubisco activase (AA 1 -
                  473) [Arabidopsis thaliana]

```

```
Seq. No.      402208
Seq. ID      LIB3431-051-P1-K1-D6
Method       BLASTX
NCBI GI      g2072555
BLAST score   150
E value      3.0e-10
Match length  30
% identity    90
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
               >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
               protein [Oryza sativa]
```

```
Seq. No.      402209
Seq. ID      LIB3431-051-P1-K1-D7
Method       BLASTN
NCBI GI      g3377792
BLAST score   106
E value      2.0e-52
Match length  309
% identity    84
NCBI Description  Oryza sativa ribulose-1,5-bisphosphate
                  carboxylase/oxygenase activase (rca) mRNA, complete cds
```

```
Seq. No.      402210
Seq. ID      LIB3431-051-P1-K1-D8
Method       BLASTN
NCBI GI      g3821780
BLAST score   36
E value      1.0e-10
Match length  47
% identity    66
NCBI Description  Xenopus laevis cDNA clone 27A6-1
```

```
Seq. No.          402211
Seq. ID           LIB3431-051-P1-K1-D9
Method            BLASTX
NCBI GI           g131388
BLAST score       264
E value           5.0e-23
Match length      108
% identity        60
NCBI Description   OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir_S16260
                  photosystem II oxygen-evolving complex protein 1 - common
                  wheat x Sanduri wheat >gi 21844 emb CAA40670 (X57408)
```


E value 6.0e-34
 Match length 104
 % identity 73
 NCBI Description (AF050674) ribosomal protein L27 precursor [Oryza sativa]

Seq. No. 402217
 Seq. ID LIB3431-051-P1-K1-E5
 Method BLASTX
 NCBI GI g4512707
 BLAST score 419
 E value 5.0e-41
 Match length 151
 % identity 54
 NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No. 402218
 Seq. ID LIB3431-051-P1-K1-E6
 Method BLASTN
 NCBI GI g505134
 BLAST score 63
 E value 5.0e-27
 Match length 163
 % identity 85
 NCBI Description Rice mRNA for ferredoxin, complete cds

Seq. No. 402219
 Seq. ID LIB3431-051-P1-K1-E8
 Method BLASTX
 NCBI GI g320618
 BLAST score 303
 E value 4.0e-28
 Match length 61
 % identity 92
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 402220
 Seq. ID LIB3431-051-P1-K1-E9
 Method BLASTX
 NCBI GI g1617197
 BLAST score 292
 E value 2.0e-26
 Match length 76
 % identity 74
 NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 402221
 Seq. ID LIB3431-051-P1-K1-F1
 Method BLASTX
 NCBI GI g115808
 BLAST score 472
 E value 1.0e-47
 Match length 92
 % identity 97

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 91R PRECURSOR (LHCII TYPE I CAB-91R) (LHCP) >gi_72732_pir_CDPJ91 chlorophyll a/b-binding protein 91R precursor - petunia
>gi_20487_emb_CAA26209_(X02356) cab 91R precursor polypeptide (aa -34 to 233) [Petunia sp.]

Seq. No. 402222
Seq. ID LIB3431-051-P1-K1-F10
Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 1.0e-19
Match length 44
% identity 100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_(AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 402223
Seq. ID LIB3431-051-P1-K1-F11
Method BLASTX
NCBI GI g320618
BLAST score 542
E value 2.0e-56
Match length 133
% identity 86
NCBI Description chlorophyll a/b-binding protein I precursor - rice
>gi_218172_dbj_BAA00536_(D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa]
>gi_227611_prf_1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No. 402224
Seq. ID LIB3431-051-P1-K1-F3
Method BLASTN
NCBI GI g3789951
BLAST score 254
E value 1.0e-141
Match length 297
% identity 97
NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 402225
Seq. ID LIB3431-051-P1-K1-F4
Method BLASTX
NCBI GI g3913018
BLAST score 565
E value 2.0e-58
Match length 116
% identity 94
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_(D13513) chloroplastic aldolase [Oryza sativa]

Seq. No. 402226

E value 2.0e-55
 Match length 112
 % identity 92
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 402232
 Seq. ID LIB3431-051-P1-K1-G12
 Method BLASTX
 NCBI GI g132105
 BLAST score 268
 E value 9.0e-43
 Match length 109
 % identity 82
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 402233
 Seq. ID LIB3431-051-P1-K1-G3
 Method BLASTX
 NCBI GI g5523862
 BLAST score 367
 E value 3.0e-35
 Match length 99
 % identity 69
 NCBI Description (AF085169) LRk-type protein [Triticum aestivum]

Seq. No. 402234
 Seq. ID LIB3431-051-P1-K1-G4
 Method BLASTX
 NCBI GI g3789954
 BLAST score 458
 E value 1.0e-45
 Match length 109
 % identity 83
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 402235
 Seq. ID LIB3431-051-P1-K1-G5
 Method BLASTX
 NCBI GI g82080
 BLAST score 230
 E value 3.0e-19
 Match length 76
 % identity 63
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf_1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No. 402236

light-regulated gene [Oryza sativa]

Seq. No. 402241
 Seq. ID LIB3431-051-P1-K1-H4
 Method BLASTN
 NCBI GI g3345476
 BLAST score 260
 E value 1.0e-144
 Match length 282
 % identity 99
 NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds

Seq. No. 402242
 Seq. ID LIB3431-051-P1-K1-H7
 Method BLASTX
 NCBI GI g4678947
 BLAST score 353
 E value 2.0e-33
 Match length 101
 % identity 65
 NCBI Description (AL049711) putative protein [Arabidopsis thaliana]

Seq. No. 402243
 Seq. ID LIB3431-051-P1-N1-A1
 Method BLASTX
 NCBI GI g1170606
 BLAST score 159
 E value 1.0e-10
 Match length 49
 % identity 65
 NCBI Description ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE)
 >gi_629863_pir_S45634 adenylate kinase (EC 2.7.4.3),
 chloroplast - maize >gi_3114421_pdb_1ZAK_A Chain A,
 Adenylate Kinase From Maize In Complex With The Inhibitor
 P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a)
 >gi_3114422_pdb_1ZAK_B Chain B, Adenylate Kinase From Maize
 In Complex With The Inhibitor
 P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a)

Seq. No. 402244
 Seq. ID LIB3431-051-P1-N1-A10
 Method BLASTN
 NCBI GI g2072554
 BLAST score 164
 E value 4.0e-87
 Match length 296
 % identity 89
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 402245
 Seq. ID LIB3431-051-P1-N1-A12
 Method BLASTX
 NCBI GI g2864617
 BLAST score 179
 E value 4.0e-13
 Match length 60

% identity 65
 NCBI Description (AL021811) H+-transporting ATP synthase chain9 - like protein [Arabidopsis thaliana] >gi_5730141_emb_CAB52473.1 (AJ245574) ATP synthase beta chain precursor (subunit II) [Arabidopsis thaliana]

Seq. No. 402246
 Seq. ID LIB3431-051-P1-N1-A2
 Method BLASTX
 NCBI GI g693920
 BLAST score 356
 E value 8.0e-34
 Match length 68
 % identity 100
 NCBI Description (U21113) chlorophyll a/b binding protein [Solanum tuberosum]

Seq. No. 402247
 Seq. ID LIB3431-051-P1-N1-A5
 Method BLASTN
 NCBI GI g5456937
 BLAST score 329
 E value 0.0e+00
 Match length 329
 % identity 100
 NCBI Description Oryza sativa rps9 mRNA for ribosomal protein S9, complete cds

Seq. No. 402248
 Seq. ID LIB3431-051-P1-N1-A6
 Method BLASTX
 NCBI GI g4508079
 BLAST score 350
 E value 4.0e-33
 Match length 95
 % identity 66
 NCBI Description (AC005882) 66284 [Arabidopsis thaliana]

Seq. No. 402249
 Seq. ID LIB3431-051-P1-N1-A9
 Method BLASTN
 NCBI GI g18266
 BLAST score 35
 E value 3.0e-10
 Match length 47
 % identity 94
 NCBI Description C.stellata mRNA for ribosomal protein L27

Seq. No. 402250
 Seq. ID LIB3431-051-P1-N1-B1
 Method BLASTX
 NCBI GI g132105
 BLAST score 537
 E value 5.0e-55
 Match length 99
 % identity 99
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

09634016 101000

```
Seq. No.      402252
Seq. ID       LIB3431-051-P1-N1-B11
Method        BLASTX
NCBI GI       g4538963
BLAST score   169
E value       5.0e-12
Match length  48
% identity    71
NCBI Description (AL049488) chlorophyll a/b-binding protein-like
                [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1
                (AF134129) Lhcb5 protein [Arabidopsis thaliana]
```

```
Seq. No.      402253
Seq. ID      LIB3431-051-P1-N1-B12
Method       BLASTX
NCBI GI      g733456
BLAST score   335
E value      2.0e-31
Match length  73
% identity    92
NCBI Description (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
               [Zea mays]
```

```
Seq. No.      402254
Seq. ID       LIB3431-05i-P1-N1-B4
Method        BLASTN
NCBI GI       g2072554
BLAST score   134
E value       4.0e-69
Match length  354
% identity    85
NCBI Description  Oryza sativa metallothionein-like protein mRNA, complete
                  cds
```

Seq. No.	402255
Seq. ID	LIB3431-051-P1-N1-B5
Method	BLASTX

NCBI GI g3345477
 BLAST score 172
 E value 3.0e-12
 Match length 32
 % identity 97
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 402256
 Seq. ID LIB3431-051-P1-N1-B6
 Method BLASTN
 NCBI GI g2624327
 BLAST score 240
 E value 1.0e-132
 Match length 284
 % identity 96
 NCBI Description Oryza sativa mRNA for glycine rich RNA-binding protein 2 (OsGRP2)

Seq. No. 402257
 Seq. ID LIB3431-051-P1-N1-B8
 Method BLASTX
 NCBI GI g2440046
 BLAST score 163
 E value 3.0e-11
 Match length 40
 % identity 70
 NCBI Description (AJ001294) major intrinsic protein PIPC [Craterostigma plantagineum]

Seq. No. 402258
 Seq. ID LIB3431-051-P1-N1-C1
 Method BLASTN
 NCBI GI g20191
 BLAST score 215
 E value 1.0e-117
 Match length 279
 % identity 94
 NCBI Description O.sativa mRNA for catalase

Seq. No. 402259
 Seq. ID LIB3431-051-P1-N1-C10
 Method BLASTX
 NCBI GI g5734790
 BLAST score 373
 E value 9.0e-36
 Match length 80
 % identity 90
 NCBI Description (AC007980) ATP-dependent metalloprotease [Arabidopsis thaliana]

Seq. No. 402260
 Seq. ID LIB3431-051-P1-N1-C11
 Method BLASTN
 NCBI GI g20177
 BLAST score 44
 E value 7.0e-16
 Match length 88

[Zea mays]

Seq. No. 402266
Seq. ID LIB3431-051-P1-N1-D11
Method BLASTX
NCBI GI g5106775
BLAST score 363
E value 1.0e-34
Match length 71
% identity 96
NCBI Description (AF067732) ribosomal protein S12 [Hordeum vulgare]

Seq. No. 402267
Seq. ID LIB3431-051-P1-N1-D12
Method BLASTX
NCBI GI g5106775
BLAST score 259
E value 2.0e-22
Match length 52
% identity 92
NCBI Description (AF067732) ribosomal protein S12 [Hordeum vulgare]

Seq. No. 402268
Seq. ID LIB3431-051-P1-N1-D4
Method BLASTX
NCBI GI g132166
BLAST score 160
E value 5.0e-11
Match length 31
% identity 87
NCBI Description RIBULOSE BISPHTHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
>gi_81660_pir_S04048 ribulose-bisphosphate carboxylase
activase precursor - Arabidopsis thaliana
>gi_16471_emb_CAA32429_(X14212) rubisco activase (AA 1 -
473) [Arabidopsis thaliana]

Seq. No. 402269
Seq. ID LIB3431-051-P1-N1-D5
Method BLASTX
NCBI GI g167097
BLAST score 142
E value 7.0e-09
Match length 30
% identity 83
NCBI Description (M55449) ribulose 1,5-bisphosphate carboxylase activase
[Hordeum vulgare]

Seq. No. 402270
Seq. ID LIB3431-051-P1-N1-D6
Method BLASTN
NCBI GI g3377792
BLAST score 97
E value 4.0e-47
Match length 267
% identity 84
NCBI Description Oryza sativa ribulose-1,5-bisphosphate

carboxylase/oxygenase activase (rca) mRNA, complete cds

Seq. No. 402271
 Seq. ID LIB3431-051-P1-N1-D8
 Method BLASTN
 NCBI GI g416266
 BLAST score 211
 E value 1.0e-115
 Match length 269
 % identity 94
 NCBI Description Rice mRNA for oxygen-evolving protein, partial sequence

Seq. No. 402272
 Seq. ID LIB3431-051-P1-N1-D9
 Method BLASTX
 NCBI GI g733454
 BLAST score 158
 E value 8.0e-11
 Match length 45
 % identity 69
 NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No. 402273
 Seq. ID LIB3431-051-P1-N1-E1
 Method BLASTX
 NCBI GI g2961176
 BLAST score 322
 E value 7.0e-30
 Match length 81
 % identity 80
 NCBI Description (AF050674) ribosomal protein L27 precursor [Oryza sativa]

Seq. No. 402274
 Seq. ID LIB3431-051-P1-N1-E10
 Method BLASTX
 NCBI GI g3928140
 BLAST score 166
 E value 1.0e-11
 Match length 34
 % identity 88
 NCBI Description (AJ131044) chlorophyll a/b binding protein [Cicer arietinum]

Seq. No. 402275
 Seq. ID LIB3431-051-P1-N1-E5
 Method BLASTX
 NCBI GI g1070408
 BLAST score 166
 E value 1.0e-11
 Match length 47
 % identity 74
 NCBI Description ferredoxin [2Fe-2S] I - rice

Seq. No. 402276
 Seq. ID LIB3431-051-P1-N1-E7
 Method BLASTX

NCBI GI g115786
 BLAST score 202
 E value 8.0e-16
 Match length 52
 % identity 75
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi_82680_pir_A29119 chlorophyll a/b-binding protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea mays]

Seq. No. 402277
 Seq. ID LIB3431-051-P1-N1-E9
 Method BLASTN
 NCBI GI g5917782
 BLAST score 139
 E value 2.0e-72
 Match length 228
 % identity 89
 NCBI Description Oryza sativa carbonic anhydrase 3 mRNA, complete cds

Seq. No. 402278
 Seq. ID LIB3431-051-P1-N1-F10
 Method BLASTX
 NCBI GI g3036949
 BLAST score 262
 E value 7.0e-23
 Match length 53
 % identity 94
 NCBI Description (AB012638) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 402279
 Seq. ID LIB3431-051-P1-N1-F2
 Method BLASTN
 NCBI GI g3789951
 BLAST score 136
 E value 2.0e-70
 Match length 311
 % identity 99
 NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 402280
 Seq. ID LIB3431-051-P1-N1-F8
 Method BLASTX
 NCBI GI g551047
 BLAST score 241
 E value 2.0e-20
 Match length 50
 % identity 90
 NCBI Description (X79277) type II LHCI [Lolium temulentum]

Seq. No. 402281
 Seq. ID LIB3431-051-P1-N1-F9
 Method BLASTN
 NCBI GI g2306980

BLAST score 180
 E value 9.0e-97
 Match length 240
 % identity 94
 NCBI Description Oryza sativa photosystem I antenna protein (Lhca) mRNA, complete cds

Seq. No. 402282
 Seq. ID LIB3431-051-P1-N1-G10
 Method BLASTX
 NCBI GI g3126854
 BLAST score 270
 E value 1.0e-23
 Match length 52
 % identity 98
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 402283
 Seq. ID LIB3431-051-P1-N1-G11
 Method BLASTX
 NCBI GI g671740
 BLAST score 170
 E value 5.0e-12
 Match length 41
 % identity 83
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 402284
 Seq. ID LIB3431-051-P1-N1-G12
 Method BLASTX
 NCBI GI g132105
 BLAST score 167
 E value 1.0e-11
 Match length 33
 % identity 97
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR ... (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 402285
 Seq. ID LIB3431-051-P1-N1-G2
 Method BLASTX
 NCBI GI g5679314
 BLAST score 317
 E value 3.0e-29
 Match length 100
 % identity 66
 NCBI Description (AF164021) receptor kinase [Oryza sativa]

Seq. No. 402286

09684016.101000

Seq. ID	LIB3431-051-P1-N1-G3
Method	BLASTN
NCBI GI	g3789953
BLAST score	39
E value	1.0e-12
Match length	43
% identity	98
NCBI Description	Oryza sativa chlorophyll a/b-binding protein precursor (Cab26) mRNA, nuclear gene encoding chloroplast protein, complete cds
Seq. No.	402287
Seq. ID	LIB3431-051-P1-N1-G6
Method	BLASTX
NCBI GI	g1617197
BLAST score	225
E value	2.0e-18
Match length	47
% identity	87
NCBI Description	(272488) CP12 [Nicotiana tabacum]
Seq. No.	402288
Seq. ID	LIB3431-051-P1-N1-G8
Method	BLASTN
NCBI GI	g20369
BLAST score	292
E value	1.0e-163
Match length	308
% identity	99
NCBI Description	Oryza sativa shoot GS2 mRNA for chloroplastic glutamine synthetase (EC 6.3.1.2) (clone lambda-GS31) >gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of chloroplast localising glutamine synthetase
Seq. No.	402289
Seq. ID	LIB3431-051-P1-N1-H1
Method	BLASTN
NCBI GI	g1519250
BLAST score	385
E value	0.0e+00
Match length	421
% identity	98
NCBI Description	Oryza sativa GF14-c protein mRNA, complete cds
Seq. No.	402290
Seq. ID	LIB3431-051-P1-N1-H10
Method	BLASTX
NCBI GI	g133936
BLAST score	610
E value	1.0e-63
Match length	125
% identity	97
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi_70867_pir_R3RZ3 ribosomal protein S3 - rice chloroplast >gi_12025_emb_CAA33934_(X15901) ribosomal protein S3 [Oryza sativa] >gi_226646_prf_1603356BW ribosomal protein S3 [Oryza sativa]

thaliana]

Seq. No. 402296
 Seq. ID LIB3431-052-P1-K1-A12
 Method BLASTN
 NCBI GI g6015437
 BLAST score 41
 E value 6.0e-14
 Match length 52
 % identity 68
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 402297
 Seq. ID LIB3431-052-P1-K1-A4
 Method BLASTX
 NCBI GI g131225
 BLAST score 308
 E value 2.0e-28
 Match length 70
 % identity 87
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 402298
 Seq. ID LIB3431-052-P1-K1-A8
 Method BLASTX
 NCBI GI g168643
 BLAST score 260
 E value 7.0e-23
 Match length 83
 % identity 65
 NCBI Description (L02540) NADPH HC-toxin reductase [Zea mays]

Seq. No. 402299
 Seq. ID LIB3431-052-P1-K1-B11
 Method BLASTN
 NCBI GI g2062705
 BLAST score 36
 E value 9.0e-11
 Match length 36
 % identity 100
 NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 402300
 Seq. ID LIB3431-052-P1-K1-B12
 Method BLASTX
 NCBI GI g3158476
 BLAST score 230
 E value 2.0e-19
 Match length 62
 % identity 71
 NCBI Description (AF067185) aquaporin 2 [Samanea saman]

Seq. No. 402301
 Seq. ID LIB3431-052-P1-K1-B4

NCBI GI g3789952
 BLAST score 341
 E value 5.0e-32
 Match length 66
 % identity 98
 NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No. 402326
 Seq. ID LIB3431-052-P1-K1-F2
 Method BLASTX
 NCBI GI g3075488
 BLAST score 303
 E value 9.0e-28
 Match length 82
 % identity 72
 NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 402327
 Seq. ID LIB3431-052-P1-K1-F4
 Method BLASTN
 NCBI GI g4959460
 BLAST score 33
 E value 3.0e-09
 Match length 33
 % identity 100
 NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No. 402328
 Seq. ID LIB3431-052-P1-K1-F5
 Method BLASTX
 NCBI GI g3360289
 BLAST score 230
 E value 4.0e-19
 Match length 59
 % identity 76
 NCBI Description (AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No. 402329
 Seq. ID LIB3431-052-P1-K1-F7
 Method BLASTX
 NCBI GI g5302772
 BLAST score 148
 E value 1.0e-09
 Match length 83
 % identity 40
 NCBI Description (Z97336) SNF1 like protein kinase [Arabidopsis thaliana]

Seq. No. 402330
 Seq. ID LIB3431-052-P1-K1-F8
 Method BLASTX
 NCBI GI g2129622
 BLAST score 296
 E value 5.0e-27
 Match length 71
 % identity 77

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Seq. No.      402356
Seq. ID      LIB3431-052-P1-N1-C2
Method       BLASTX
NCBI GI      g2982456
BLAST score   312
E value      2.0e-28
Match length  90
% identity    68
NCBI Description (AL022223) putative protein [Arabidopsis thaliana]
```

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Seq. No.          402358
Seq. ID           LIB3431-052-P1-N1-C4
Method            BLASTX
NCBI GI           g399333
BLAST score       205
E value           5.0e-16
Match length      44
% identity        89
NCBI Description   CYSTEINE SYNTHASE, CHLOROPLAST PRECURSOR (O-ACETYL SERINE
                  SULFHYDRYLASE) (O-ACETYL SERINE (THIOL)-LYASE) (CSASE)
                  >gi_322740_pir_A43407 cysteine synthase (EC 4.2.99.8)
                  precursor - pepper >gi_17944_emb_CAA46086_ (X64874)
                  O-acetylserine (thiol)-lyase [Capsicum annuum]
```

51673

E value 8.0e-18
 Match length 55
 % identity 78
 NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf_1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No. 402365
 Seq. ID LIB3431-052-P1-N1-D6
 Method BLASTX
 NCBI GI g671740
 BLAST score 426
 E value 7.0e-42
 Match length 77
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 402366
 Seq. ID LIB3431-052-P1-N1-D7
 Method BLASTX
 NCBI GI g4335763
 BLAST score 167
 E value 1.0e-11
 Match length 75
 % identity 45
 NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]

Seq. No. 402367
 Seq. ID LIB3431-052-P1-N1-D9
 Method BLASTX
 NCBI GI g4566614
 BLAST score 306
 E value 9.0e-28
 Match length 69
 % identity 84
 NCBI Description (AF112887) actin depolymerizing factor [Populus alba x Populus tremula]

Seq. No. 402368
 Seq. ID LIB3431-052-P1-N1-E1
 Method BLASTN
 NCBI GI g218207
 BLAST score 295
 E value 1.0e-165
 Match length 295
 % identity 100
 NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139

Seq. No. 402369
 Seq. ID LIB3431-052-P1-N1-E12
 Method BLASTX
 NCBI GI g3510256
 BLAST score 298
 E value 6.0e-27

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 402375
Seq. ID LIB3431-052-P1-N1-E7
Method BLASTX
NCBI GI g671740
BLAST score 346
E value 9.0e-33
Match length 76
% identity 84
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 402376
Seq. ID LIB3431-052-P1-N1-E9
Method BLASTX
NCBI GI g1173347
BLAST score 331
E value 1.0e-30
Match length 82
% identity 83
NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]

Seq. No. 402377
Seq. ID LIB3431-052-P1-N1-F10
Method BLASTN
NCBI GI g3789951
BLAST score 77
E value 3.0e-35
Match length 245
% identity 82
NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor (Cab27) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 402378
Seq. ID LIB3431-052-P1-N1-F11
Method BLASTX
NCBI GI g21839
BLAST score 343
E value 4.0e-32
Match length 72
% identity 94
NCBI Description (X57952) phosphoribulokinase [Triticum aestivum]

Seq. No. 402379
Seq. ID LIB3431-052-P1-N1-F12
Method BLASTN
NCBI GI g21838
BLAST score 36
E value 1.0e-10
Match length 139

% identity 79
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
 >gi_226872_prf_1609235A chlorophyll a/b binding protein
 [Lycopersicon esculentum]

Seq. No. 402385
 Seq. ID LIB3431-052-P1-N1-G3
 Method BLASTX
 NCBI GI g2501190
 BLAST score 470
 E value 5.0e-47
 Match length 117
 % identity 83
 NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
 >gi_2130147_pir_S61420 thiamine biosynthetic enzyme thil-2
 - maize >gi_596080 (U17351) thiamine biosynthetic enzyme
 [Zea mays]

Seq. No. 402386
 Seq. ID LIB3431-052-P1-N1-G8
 Method BLASTN
 NCBI GI g21838
 BLAST score 70
 E value 5.0e-31
 Match length 207
 % identity 85
 NCBI Description T.aestivum PRK gene for ribulose-5-phosphate kinase

Seq. No. 402387
 Seq. ID LIB3431-052-P1-N1-G9
 Method BLASTX
 NCBI GI g693920
 BLAST score 403
 E value 4.0e-39
 Match length 77
 % identity 99
 NCBI Description (U21113) chlorophyll a/b binding protein [Solanum
 tuberosum]

Seq. No. 402388
 Seq. ID LIB3431-052-P1-N1-H1
 Method BLASTX
 NCBI GI g115787
 BLAST score 495
 E value 6.0e-50
 Match length 98
 % identity 97
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
 protein 2R precursor - rice >gi_20182_emb_CAA32109
 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
 [Oryza sativa]

Seq. No. 402389
 Seq. ID LIB3431-052-P1-N1-H10
 Method BLASTX
 NCBI GI g82080

BLAST score 291
 E value 4.0e-26
 Match length 71
 % identity 82
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
 >gi_226872_prf_1609235A chlorophyll a/b binding protein
 [Lycopersicon esculentum]

Seq. No. 402390
 Seq. ID LIB3431-052-P1-N1-H11
 Method BLASTX
 NCBI GI g119194
 BLAST score 270
 E value 9.0e-24
 Match length 62
 % identity 85
 NCBI Description ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)
 >gi_81607_pir_S09152 translation elongation factor Tu
 precursor, chloroplast - Arabidopsis thaliana
 >gi_22565_emb_CAA36498_(X52256) elongation factor Tu
 precursor [Arabidopsis thaliana]
 >gi_5738381_emb_CAB45802.2_(AL080253) translation
 elongation factor EF-Tu precursor, chloroplast [Arabidopsis
 thaliana] >gi_226817_prf_1607332A elongation factor Tu
 [Arabidopsis thaliana]

Seq. No. 402391
 Seq. ID LIB3431-052-P1-N1-H2
 Method BLASTX
 NCBI GI g226263
 BLAST score 158
 E value 1.0e-10
 Match length 29
 % identity 97
 NCBI Description chlorophyll a/b binding protein [Glycine max]

Seq. No. 402392
 Seq. ID LIB3431-052-P1-N1-H3
 Method BLASTX
 NCBI GI g3789954
 BLAST score 237
 E value 7.0e-20
 Match length 44
 % identity 95
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza
 sativa]

Seq. No. 402393
 Seq. ID LIB3431-052-P1-N1-H5
 Method BLASTN
 NCBI GI g14264
 BLAST score 60
 E value 5.0e-25
 Match length 100
 % identity 90
 NCBI Description T.aestivum gene for sedoheptulose-1,7-bisphosphatase

Seq. No. 402394
 Seq. ID LIB3431-052-P1-N1-H7
 Method BLASTX
 NCBI GI g131176
 BLAST score 251
 E value 1.0e-21
 Match length 48
 % identity 98
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR
 (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
 >gi_72683_pir_F1BH4 photosystem I chain IV precursor -
 barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA
 -46 to 101) [Hordeum vulgare] >gi_226163_prf_1413233A
 10.8kD photosystem I protein [Hordeum vulgare var.
 distichum]

Seq. No. 402395
 Seq. ID LIB3431-052-P1-N1-H9
 Method BLASTX
 NCBI GI g3183079
 BLAST score 209
 E value 1.0e-16
 Match length 54
 % identity 76
 NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
 >gi_1375075_dbj_BAA12870.1_ (D85763) glyoxysomal malate
 dehydrogenase [Oryza sativa]

Seq. No. 402396
 Seq. ID LIB3431-053-P1-K1-A1
 Method BLASTX
 NCBI GI g871931
 BLAST score 387
 E value 2.0e-37
 Match length 78
 % identity 99
 NCBI Description (D30763) ferredoxin [Oryza sativa]

Seq. No. 402397
 Seq. ID LIB3431-053-P1-K1-A10
 Method BLASTX
 NCBI GI g729479
 BLAST score 667
 E value 1.0e-72
 Match length 147
 % identity 82
 NCBI Description FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) >gi_551131
 (U14956) ferredoxin NADP+ reductase precursor [Vicia faba]

Seq. No. 402398
 Seq. ID LIB3431-053-P1-K1-A11
 Method BLASTX
 NCBI GI g131225
 BLAST score 322
 E value 3.0e-30
 Match length 71
 % identity 87

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 402399
 Seq. ID LIB3431-053-P1-K1-A12
 Method BLASTX
 NCBI GI g4585882
 BLAST score 638
 E value 8.0e-67
 Match length 143
 % identity 79
 NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No. 402400
 Seq. ID LIB3431-053-P1-K1-A2
 Method BLASTX
 NCBI GI g2894534
 BLAST score 392
 E value 4.0e-38
 Match length 103
 % identity 77
 NCBI Description (AJ224327) aquaporin [Oryza sativa]

Seq. No. 402401
 Seq. ID LIB3431-053-P1-K1-A3
 Method BLASTX
 NCBI GI g4038699
 BLAST score 198
 E value 3.0e-23
 Match length 65
 % identity 82
 NCBI Description (AB020947) ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit [Aegilops speltoides]

Seq. No. 402402
 Seq. ID LIB3431-053-P1-K1-A6
 Method BLASTX
 NCBI GI g417154
 BLAST score 429
 E value 3.0e-42
 Match length 135
 % identity 63
 NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir_S25541 heat shock protein 82 - rice (strain Taichung Native One) >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]

Seq. No. 402403
 Seq. ID LIB3431-053-P1-K1-A7
 Method BLASTX
 NCBI GI g2407281
 BLAST score 399
 E value 5.0e-39
 Match length 81

Seq. No. 402413
 Seq. ID LIB3431-053-P1-K1-B9
 Method BLASTX
 NCBI GI g1835731
 BLAST score 319
 E value 1.0e-29
 Match length 66
 % identity 95
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 402414
 Seq. ID LIB3431-053-P1-K1-C1
 Method BLASTX
 NCBI GI g5734636
 BLAST score 297
 E value 8.0e-27
 Match length 106
 % identity 50
 NCBI Description (AP000391) Similar to putative lipase (AC006232) [Oryza sativa]

Seq. No. 402415
 Seq. ID LIB3431-053-P1-K1-C11
 Method BLASTX
 NCBI GI g2130042
 BLAST score 688
 E value 1.0e-72
 Match length 149
 % identity 92
 NCBI Description Mg-chelatase chain Xantha-f - barley >gi_861199 (U26916) protoporphyrin IX Mg-chelatase subunit precursor [Hordeum vulgare]

Seq. No. 402416
 Seq. ID LIB3431-053-P1-K1-C12
 Method BLASTX
 NCBI GI g115772
 BLAST score 675
 E value 4.0e-71
 Match length 136
 % identity 94
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi_82460_pir_S03705 chlorophyll a/b-binding protein 1R precursor - rice >gi_20178_emb_CAA32108 (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235) [Oryza sativa]

Seq. No. 402417
 Seq. ID LIB3431-053-P1-K1-C2
 Method BLASTX
 NCBI GI g2072555
 BLAST score 194
 E value 6.0e-15
 Match length 52
 % identity 73
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

0964016 100000

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Seq. No.          402419
Seq. ID           LIB3431-053-P1-K1-C4
Method            BLASTN
NCBI GI           g6015437
BLAST score       36
E value           2.0e-10
Match length      36
% identity        100
NCBI Description   Homo sapiens PEX1 mRNA, complete cds
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Seq. No.          402421
Seq. ID           LIB3431-053-P1-K1-C6
Method            BLASTX
NCBI GI           g82734
BLAST score       812
E value           4.0e-87
Match length      164
% identity        31
NCBI Description   ubiquitin precursor - maize (fragment)
                   >gi 226763 prf 1604470A poly-ubiquitin [Zea mays]
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51686

Match length 102
 % identity 84
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 402423
 Seq. ID LIB3431-053-P1-K1-D10
 Method BLASTX
 NCBI GI g548605
 BLAST score 488
 E value 3.0e-49
 Match length 113
 % identity 87
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
 (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
 >gi_539055_pir_A48527 photosystem I protein psaK precursor
 - barley >gi_304220 (L12707) photosystem I PSI-K subunit
 [Hordeum vulgare]

Seq. No. 402424
 Seq. ID LIB3431-053-P1-K1-D12
 Method BLASTX
 NCBI GI g3288821
 BLAST score 422
 E value 2.0e-41
 Match length 106
 % identity 75
 NCBI Description (AF063901) alanine:glyoxylate aminotransferase;
 transaminase [Arabidopsis thaliana]
 >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209)
 alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

Seq. No. 402425
 Seq. ID LIB3431-053-P1-K1-D2
 Method BLASTN
 NCBI GI g5852170
 BLAST score 86
 E value 2.0e-40
 Match length 130
 % identity 46
 NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC
 clone:tl17804

Seq. No. 402426
 Seq. ID LIB3431-053-P1-K1-D3
 Method BLASTX
 NCBI GI g4972052
 BLAST score 372
 E value 1.0e-35
 Match length 134
 % identity 40
 NCBI Description (AL078470) putative protein [Arabidopsis thaliana]

Seq. No. 402427

NCBI GI g3885891
 BLAST score 171
 E value 2.0e-91
 Match length 209
 % identity 96
 NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds

Seq. No. 402433
 Seq. ID LIB3431-053-P1-K1-E11
 Method BLASTX
 NCBI GI g4544390
 BLAST score 364
 E value 1.0e-34
 Match length 141
 % identity 52
 NCBI Description (AC007047) hypothetical protein [Arabidopsis thaliana]

Seq. No. 402434
 Seq. ID LIB3431-053-P1-K1-E12
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 1.0e-19
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 402435
 Seq. ID LIB3431-053-P1-K1-E2
 Method BLASTN
 NCBI GI g218209
 BLAST score 66
 E value 2.0e-28
 Match length 94
 % identity 93
 NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No. 402436
 Seq. ID LIB3431-053-P1-K1-E3
 Method BLASTX
 NCBI GI g2072727
 BLAST score 736
 E value 3.0e-78
 Match length 143
 % identity 99
 NCBI Description (Y12595) Fd-GOGAT protein [Oryza sativa]

Seq. No. 402437
 Seq. ID LIB3431-053-P1-K1-E4
 Method BLASTN
 NCBI GI g3821780
 BLAST score 35

E value 7.0e-11
 Match length 35
 % identity 100
 NCBI Description *Xenopus laevis* cDNA clone 27A6-1

Seq. No. 402438
 Seq. ID LIB3431-053-P1-K1-E5
 Method BLASTN
 NCBI GI g3821780
 BLAST score 35
 E value 8.0e-11
 Match length 35
 % identity 100
 NCBI Description *Xenopus laevis* cDNA clone 27A6-1

Seq. No. 402439
 Seq. ID LIB3431-053-P1-K1-E6
 Method BLASTX
 NCBI GI g131388
 BLAST score 403
 E value 3.0e-39
 Match length 131
 % identity 67
 NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir_S16260
 photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670 (X57408)
 33kDa oxygen evolving protein of photosystem II [*Triticum aestivum*]

Seq. No. 402440
 Seq. ID LIB3431-053-P1-K1-E7
 Method BLASTX
 NCBI GI g4417296
 BLAST score 368
 E value 3.0e-35
 Match length 102
 % identity 68
 NCBI Description (AC007019) unknown protein [*Arabidopsis thaliana*]
 >gi_4587592_gb_AAD25820.1_AC007232_10 (AC007232) unknown protein [*Arabidopsis thaliana*]

Seq. No. 402441
 Seq. ID LIB3431-053-P1-K1-E9
 Method BLASTX
 NCBI GI g3885894
 BLAST score 463
 E value 2.0e-46
 Match length 104
 % identity 88
 NCBI Description (AF093635) photosystem-1 H subunit GOS5 [*Oryza sativa*]

Seq. No. 402442
 Seq. ID LIB3431-053-P1-K1-F1
 Method BLASTX
 NCBI GI g2570511

09684016-101000

dehydrogenase. (M64118) [Oryza sativa]

Seq. No. 402447
Seq. ID LIB3431-053-P1-K1-F8
Method BLASTN
NCBI GI g4835587
BLAST score 67
E value 1.0e-29
Match length 67
% identity 100
NCBI Description Oryza sativa ONIT4 mRNA for nitrilase-like protein,
complete cds

Seq. No. 402448
Seq. ID LIB3431-053-P1-K1-F9
Method BLASTX
NCBI GI g733456
BLAST score 631
E value 6.0e-66
Match length 141
% identity 85
NCBI Description (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
[Zea mays]

Seq. No. 402449
Seq. ID LIB3431-053-P1-K1-G1
Method BLASTX
NCBI GI g3047064
BLAST score 406
E value 1.0e-39
Match length 143
% identity 57
NCBI Description (AF058825) contains similarity to peptidyl-prolyl cis-trans
isomerase (Pfam: pro_isomerase.hmm, score: 23.86 and 28.41
[Arabidopsis thaliana])

Seq. No. 402450
Seq. ID LIB3431-053-P1-K1-G10
Method BLASTX
NCBI GI g671740
BLAST score 338
E value 2.0e-31
Match length 63
% identity 98
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
construct]

Seq. No. 402451
Seq. ID LIB3431-053-P1-K1-G11
Method BLASTX
NCBI GI g132105
BLAST score 653
E value 2.0e-68
Match length 141
% identity 88
NCBI Description RUBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9

066401E-101000

```
Seq. No.      402457
Seq. ID      LIB3431-053-P1-K1-G9
Method       BLASTX
NCBI GI      g82080
BLAST score   535
E value      1.0e-54
Match length  148
% identity    69
NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
                  >gi_226872_prf_1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
```

```
Seq. No.      402459
Seq. ID      LIB3431-053-P1-K1-H11
Method       BLASTN
NCBI GI      g4680178
BLAST score   84
E value      3.0e-39
Match length  129
% identity    90
NCBI Description  Oryza sativa subsp. indica Retrosat 1 retrotransposon and
                  Ty3-Gypsy type Retrosat 2 retrotransposon, complete
```

sequences; and unknown genes

Seq. No. 402460
Seq. ID LIB3431-053-P1-K1-H2
Method BLASTX
NCBI GI g733454
BLAST score 357
E value 6.0e-34
Match length 101
% identity 72
NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No. 402461
Seq. ID LIB3431-053-P1-K1-H3
Method BLASTX
NCBI GI g4582459
BLAST score 329
E value 1.0e-30
Match length 98
% identity 63
NCBI Description (AC007071) putative RanBP7/importin protein [Arabidopsis thaliana]

Seq. No. 402462
Seq. ID LIB3431-053-P1-K1-H6
Method BLASTX
NCBI GI g2570496
BLAST score 118
E value 1.0e-59
Match length 126
% identity 98
NCBI Description Oryza sativa H protein subunit of glycine decarboxylase mRNA, complete cds

Seq. No. 402463
Seq. ID LIB3431-053-P1-K1-H7
Method BLASTX
NCBI GI g5442410
BLAST score 380
E value 2.0e-36
Match length 133
% identity 58
NCBI Description (AF159254) ascorbate peroxidase [Zantedeschia aethiopica]

Seq. No. 402464
Seq. ID LIB3431-053-P1-K1-H8
Method BLASTX
NCBI GI g2407281
BLAST score 661
E value 2.0e-69
Match length 129
% identity 94
NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 402465

```
Seq. ID      LIB3431-053-P1-K1-H9
Method       BLASTX
NCBI GI      g3789952
BLAST score  469
E value      4.0e-47
Match length 107
% identity   87
NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza
sativa]
```

```
Seq. No.      402466
Seq. ID      LIB3431-053-P1-N1-A1
Method       BLASTN
NCBI GI      g218209
BLAST score   214
E value      1.0e-117
Match length  302
% identity    93
NCBI Description  Oryza sativa mRNA for the small subunit of
ribulose-1,5-bisphosphate carboxylase, complete cds, clone
pOSSS2106
```

```
Seq. No.          402467
Seq. ID           LIB3431-053-P1-N1-A10
Method            BLASTX
NCBI GI           g729477
BLAST score       498
E value           3.0e-50
Match length      110
% identity        84
NCBI Description  FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR)
                  >gi_320548_pir__A44974 ferredoxin--NADP+ reductase (EC
                  1.18.1.2) precursor - common ice plant >gi_167256 (M25528)
                  ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1)
                  [Mesembryanthemum crystallinum] >gi_226768_prf__1604475A
                  ferredoxin NADP reductase [Mesembryanthemum crystallinum]
```

```
Seq. No.      402468
Seq. ID      LIB3431-053-P1-N1-A11
Method       BLASTX
NCBI GI      g131225
BLAST score   179
E value      4.0e-13
Match length  48
% identity    69
NCBI Description  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein
precursor - barley >gi_167087 (M61146) photosystem I
hydrophobic protein [Hordeum vulgare]
```

Seq. No.	402469
Seq. ID	LIB3431-053-P1-N1-A12
Method	BLASTX
NCBI GI	g115813
BLAST score	211
E value	8.0e-25
Match length	82

Seq. No. 402474
 Seq. ID LIB3431-053-P1-N1-A9
 Method BLASTX
 NCBI GI g2407281
 BLAST score 266
 E value 2.0e-23
 Match length 67
 % identity 75
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [*Oryza sativa*]

Seq. No. 402475
 Seq. ID LIB3431-053-P1-N1-B10
 Method BLASTX
 NCBI GI g3036942
 BLAST score 181
 E value 3.0e-13
 Match length 37
 % identity 89
 NCBI Description (AB012636) light harvesting chlorophyll a/b-binding protein [*Nicotiana sylvestris*]

Seq. No. 402476
 Seq. ID LIB3431-053-P1-N1-B11
 Method BLASTX
 NCBI GI g347451
 BLAST score 229
 E value 9.0e-19
 Match length 48
 % identity 92
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [*Oryza sativa*]

Seq. No. 402477
 Seq. ID LIB3431-053-P1-N1-B12
 Method BLASTX
 NCBI GI g115813
 BLAST score 212
 E value 8.0e-17
 Match length 75
 % identity 61
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [*Lycopersicon esculentum*]

Seq. No. 402478
 Seq. ID LIB3431-053-P1-N1-B2
 Method BLASTX
 NCBI GI g2499819
 BLAST score 215
 E value 1.0e-30
 Match length 73
 % identity 86
 NCBI Description ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR >gi_2130068_pir_S66516 aspartic proteinase 1 precursor - rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease [*Oryza sativa*] >gi_1711289_dbj_BAA06875_ (D32144) aspartic

protease [Oryza sativa]

Seq. No. 402479
 Seq. ID LIB3431-053-P1-N1-B3
 Method BLASTX
 NCBI GI g4982478
 BLAST score 168
 E value 1.0e-11
 Match length 47
 % identity 68
 NCBI Description (AF069441) putative leucyl tRNA synthetase [Arabidopsis thaliana]

Seq. No. 402480
 Seq. ID LIB3431-053-P1-N1-B4
 Method BLASTX
 NCBI GI g421916
 BLAST score 237
 E value 5.0e-20
 Match length 49
 % identity 90
 NCBI Description chlorophyll a/b-binding protein - English ivy (fragment)
 >gi_12582_emb_CAA48410_ (X68333) light harvesting
 chlorophyll a /b binding protein [Hedera helix]

Seq. No. 402481
 Seq. ID LIB3431-053-P1-N1-B8
 Method BLASTX
 NCBI GI g400983
 BLAST score 250
 E value 3.0e-21
 Match length 70
 % identity 69
 NCBI Description 50S RIBOSOMAL PROTEIN L11, CHLOROPLAST PRECURSOR (CL11)
 >gi_279648_pir_R5SP11 ribosomal protein L11 precursor -
 spinach >gi_21313_emb_CAA39950_ (X56615) ribosomal protein
 L11 [Spinacia oleracea]

Seq. No. 402482
 Seq. ID LIB3431-053-P1-N1-B9
 Method BLASTX
 NCBI GI g1835731
 BLAST score 230
 E value 5.0e-19
 Match length 55
 % identity 82
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 402483
 Seq. ID LIB3431-053-P1-N1-C10
 Method BLASTX
 NCBI GI g687677
 BLAST score 235
 E value 1.0e-19
 Match length 51
 % identity 88
 NCBI Description (U19925) unknown [Arabidopsis thaliana]

Seq. No. 402484
 Seq. ID LIB3431-053-P1-N1-C11
 Method BLASTX
 NCBI GI g2130042
 BLAST score 317
 E value 3.0e-32
 Match length 100
 % identity 75
 NCBI Description Mg-chelatase chain Xantha-f - barley >gi_861199 (U26916)
 protoporphyrin IX Mg-chelatase subunit precursor [Hordeum
 vulgare]

Seq. No. 402485
 Seq. ID LIB3431-053-P1-N1-C12
 Method BLASTX
 NCBI GI g2645999
 BLAST score 219
 E value 8.0e-18
 Match length 56
 % identity 73
 NCBI Description (AF034631) chlorophyll a/b binding protein of LHCII type I
 precursor [Panax ginseng]

Seq. No. 402486
 Seq. ID LIB3431-053-P1-N1-C2
 Method BLASTX
 NCBI GI g2072555
 BLAST score 217
 E value 2.0e-17
 Match length 44
 % identity 93
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 402487
 Seq. ID LIB3431-053-P1-N1-C3
 Method BLASTX
 NCBI GI g671740
 BLAST score 245
 E value 1.0e-20
 Match length 49
 % identity 96
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
 construct]

Seq. No. 402488
 Seq. ID LIB3431-053-P1-N1-C5
 Method BLASTX
 NCBI GI g1835731
 BLAST score 459
 E value 1.0e-45
 Match length 102
 % identity 86
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 402489
 Seq. ID LIB3431-053-P1-N1-C6
 Method BLASTX
 NCBI GI g170354
 BLAST score 422
 E value 2.0e-41
 Match length 85
 % identity 21
 NCBI Description (M74156) pentameric polyubiquitin [*Nicotiana sylvestris*]

Seq. No. 402490
 Seq. ID LIB3431-053-P1-N1-C8
 Method BLASTX
 NCBI GI g289920
 BLAST score 319
 E value 2.0e-29
 Match length 61
 % identity 100
 NCBI Description (L07119) chlorophyll A/B binding protein [*Gossypium hirsutum*]

Seq. No. 402491
 Seq. ID LIB3431-053-P1-N1-D10
 Method BLASTN
 NCBI GI g304219
 BLAST score 52
 E value 2.0e-20
 Match length 80
 % identity 91
 NCBI Description *Hordeum vulgare* chloroplast photosystem I PSK-I subunit mRNA, complete cds

Seq. No. 402492
 Seq. ID LIB3431-053-P1-N1-D12
 Method BLASTX
 NCBI GI g2754849
 BLAST score 192
 E value 2.0e-29
 Match length 74
 % identity 85
 NCBI Description (AF039000) putative serine-glyoxylate aminotransferase [*Fritillaria agrestis*]

Seq. No. 402493
 Seq. ID LIB3431-053-P1-N1-D8
 Method BLASTX
 NCBI GI g3789952
 BLAST score 196
 E value 7.0e-15
 Match length 39
 % identity 95
 NCBI Description (AF094775) chlorophyll a/b-binding protein precursor [*Oryza sativa*]

Seq. No. 402494
 Seq. ID LIB3431-053-P1-N1-E1
 Method BLASTX

% identity 99
 NCBI Description photosystem II oxygen-evolving complex protein 1 - rice
 (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
 complex protein 1 [Oryza sativa]

Seq. No. 402500
 Seq. ID LIB3431-053-P1-N1-E7
 Method BLASTX
 NCBI GI g4417296
 BLAST score 163
 E value 5.0e-22
 Match length 78
 % identity 59
 NCBI Description (AC007019) unknown protein [Arabidopsis thaliana]
 >gi_4587592_gb_AAD25820.1 AC007232_10 (AC007232) unknown
 protein [Arabidopsis thaliana]

Seq. No. 402501
 Seq. ID LIB3431-053-P1-N1-E9
 Method BLASTX
 NCBI GI g3885894
 BLAST score 330
 E value 2.0e-38
 Match length 113
 % identity 77
 NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No. 402502
 Seq. ID LIB3431-053-P1-N1-F1
 Method BLASTX
 NCBI GI g2570511
 BLAST score 163
 E value 3.0e-22
 Match length 67
 % identity 78
 NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No. 402503
 Seq. ID LIB3431-053-P1-N1-F10
 Method BLASTX
 NCBI GI g2501190
 BLAST score 167
 E value 6.0e-19
 Match length 78
 % identity 71
 NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
 >gi_2130147_pir_S61420 thiamine biosynthetic enzyme thil-2
 - maize >gi_596080 (U17351) thiamine biosynthetic enzyme
 [Zea mays]

Seq. No. 402504
 Seq. ID LIB3431-053-P1-N1-F11
 Method BLASTX
 NCBI GI g115787
 BLAST score 471
 E value 4.0e-47
 Match length 106

% identity 94
 NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
 [Zea mays]

Seq. No. 402524
 Seq. ID LIB3431-053-P1-N1-H5
 Method BLASTX
 NCBI GI g131225
 BLAST score 318
 E value 3.0e-37
 Match length 101
 % identity 81
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
 V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein
 precursor - barley >gi_167087 (M61146) photosystem I
 hydrophobic protein [Hordeum vulgare]

Seq. No. 402525
 Seq. ID LIB3431-053-P1-N1-H6
 Method BLASTX
 NCBI GI g2499417
 BLAST score 327
 E value 2.0e-30
 Match length 78
 % identity 79
 NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
 >gi_1085826_pir_S49248 H-protein - Flaveria anomala
 >gi_547558_emb_CAA85761_ (Z37524) H-protein [Flaveria
 anomala]

Seq. No. 402526
 Seq. ID LIB3431-053-P1-N1-H7
 Method BLASTX
 NCBI GI g5442410
 BLAST score 157
 E value 1.0e-15
 Match length 109
 % identity 43
 NCBI Description (AF159254) ascorbate peroxidase [Zantedeschia aethiopica]

Seq. No. 402527
 Seq. ID LIB3431-053-P1-N1-H8
 Method BLASTX
 NCBI GI g132081
 BLAST score 170
 E value 2.0e-15
 Match length 53
 % identity 84
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
 (RUBISCO SMALL SUBUNIT) >gi_68093_pir_RKRZS
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor - rice >gi_20341_emb_CAA30393_ (X07515) ribulose
 bisphosphate carboxylase [Oryza sativa]

Seq. No. 402528
 Seq. ID LIB3431-053-P1-N1-H9
 Method BLASTN

```

NCBI GI      g3789951
BLAST score   102
E value       6.0e-50
Match length  212
% identity    87
NCBI Description  Oryza sativa chlorophyll a/b-binding protein presursor
                  (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds

```

```
Seq. No.          402529
Seq. ID           LIB3431-054-P1-K1-A10
Method            BLASTX
NCBI GI           g3913426
BLAST score       784
E value           8.0e-84
Match length      164
% identity        87
NCBI Description   S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
                  (SAMDC) >gi_1532048_emb_CAA69074_(Y07766)
                  S-adenosylmethionine decarboxylase [Oryza sativa]
```

```
Seq. No.      402530
Seq. ID       LIB3431-054-P1-K1-A12
Method        BLASTX
NCBI GI       g100880 -
BLAST score    282
E value       2.0e-25
Match length   86
% identity     71
NCBI Description  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                  (phosphorylating) (EC 1.2.1.13) A, chloroplast - maize
```

```
Seq. No.          402531
Seq. ID           LIB3431-054-P1-K1-A3
Method            BLASTX
NCBI GI           g1173347
BLAST score       591
E value           2.0e-61
Match length      115
% identity        93
NCBI Description  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                  (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                  (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
```

```
Seq. No.      402532
Seq. ID      LIB3431-054-P1-K1-A4
Method       BLASTN
NCBI GI      g3241924
BLAST score   45
E value      5.0e-16
Match length  185
% identity    81
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
MNC6, complete sequence
```

Seq. No. 402533
 Seq. ID LIB3431-054-P1-K1-A8
 Method BLASTX
 NCBI GI g320618
 BLAST score 373
 E value 7.0e-36
 Match length 91
 % identity 78
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 402534
 Seq. ID LIB3431-054-P1-K1-B10
 Method BLASTX
 NCBI GI g4972093
 BLAST score 466
 E value 1.0e-46
 Match length 125
 % identity 70
 NCBI Description (AL078468) putative protein [Arabidopsis thaliana]

Seq. No. 402535
 Seq. ID LIB3431-054-P1-K1-B11
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 1.0e-19
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 402536
 Seq. ID LIB3431-054-P1-K1-B12
 Method BLASTX
 NCBI GI g132105
 BLAST score 717
 E value 6.0e-76
 Match length 152
 % identity 89
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 402537
 Seq. ID LIB3431-054-P1-K1-B2


```
Seq. ID      LIB3431-054-P1-K1-B8
Method       BLASTX
NCBI GI      g3913018
BLAST score   681
E value      6.0e-72
Match length  136
% identity    99
NCBI Description  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                  (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic
                  aldolase [Oryza sativa]
```

```
Seq. No.      402543
Seq. ID      LIB3431-054-P1-K1-B9
Method       BLASTX
NCBI GI      g3789954
BLAST score   336
E value      2.0e-31
Match length  63
% identity    98
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]
```

```
Seq. No.          402544
Seq. ID           LIB3431-054-P1-K1-C1
Method            BLASTX
NCBI GI           g167097
BLAST score       151
E value           1.0e-21
Match length      64
% identity        84
NCBI Description   (M55449) ribulose 1,5-bisphosphate carboxylase activase
                  [Hordeum vulgare]
```

Seq. No.	402545
Seq. ID	LIB3431-054-P1-K1-C10
Method	BLASTX
NCBI GI	g1653935
BLAST score	182
E value	3.0e-13
Match length	64
% identity	56
NCBI Description	(D90917) hypothetical protein [Synechocystis sp.]

```
Seq. No.      402546
Seq. ID      LIB3431-054-P1-K1-C11
Method       BLASTX
NCBI GI      g2651310
BLAST score   375
E value      7.0e-36
Match length  148
% identity    53
NCBI Description (AC002336) putative PTR2-B peptide transporter [Arabidopsis thaliana]
```

Seq. No.	402547
Seq. ID	LIB3431-054-P1-K1-C12
Method	BLASTX

Match length 176
 % identity 92
 NCBI Description *Oryza sativa* photosystem II 10 kDa polypeptide mRNA,
 complete cds

Seq. No. 402553
 Seq. ID LIB3431-054-P1-K1-C7
 Method BLASTX
 NCBI GI g2924520
 BLAST score 609
 E value 3.0e-63
 Match length 159
 % identity 72
 NCBI Description (AL022023) plasma membrane intrinsic protein (SIMIP)
 [*Arabidopsis thaliana*]

Seq. No. 402554
 Seq. ID LIB3431-054-P1-K1-C8
 Method BLASTX
 NCBI GI g3789954
 BLAST score 628
 E value 1.0e-65
 Match length 159
 % identity 75
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [*Oryza*
sativa]

Seq. No. 402555
 Seq. ID LIB3431-054-P1-K1-C9
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 1.0e-19
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [*Oryza sativa*]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [*Oryza sativa*]

Seq. No. 402556
 Seq. ID LIB3431-054-P1-K1-D1
 Method BLASTN
 NCBI GI g2677829
 BLAST score 133
 E value 2.0e-68
 Match length 341
 % identity 85
 NCBI Description *Prunus armeniaca* ribosomal protein L12 mRNA, complete cds

Seq. No. 402557
 Seq. ID LIB3431-054-P1-K1-D10
 Method BLASTX
 NCBI GI g1778095
 BLAST score 452
 E value 4.0e-45
 Match length 122
 % identity 71

NCBI Description (U64903) putative sugar transporter; member of major facilitative superfamily; integral membrane protein [Beta vulgaris]

Seq. No. 402558
Seq. ID LIB3431-054-P1-K1-D2
Method BLASTN
NCBI GI g4138289
BLAST score 192
E value 1.0e-104
Match length 251
% identity 94
NCBI Description Oryza sativa mRNA for thioredoxin M

Seq. No. 402559
Seq. ID LIB3431-054-P1-K1-D3
Method BLASTX
NCBI GI g115796
BLAST score 571
E value 1.0e-64
Match length 127
% identity 98
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi_218174_dbj_BAA00537_ (D00642) type II light-harvesting chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 402560
Seq. ID LIB3431-054-P1-K1-D4
Method BLASTX
NCBI GI g3075488
BLAST score 518
E value 1.0e-52
Match length 117
% identity 85
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 402561
Seq. ID LIB3431-054-P1-K1-D5
Method BLASTX
NCBI GI g3789948
BLAST score 709
E value 5.0e-75
Match length 149
% identity 91
NCBI Description (AF094773) translation initiation factor 5A [Oryza sativa]

Seq. No. 402562
Seq. ID LIB3431-054-P1-K1-D7
Method BLASTX
NCBI GI g4239845
BLAST score 205
E value 6.0e-16
Match length 113
% identity 42
NCBI Description (AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No. 402578
 Seq. ID LIB3431-054-P1-K1-G11
 Method BLASTX
 NCBI GI g3757521
 BLAST score 567
 E value 2.0e-58
 Match length 169
 % identity 58
 NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

Seq. No. 402579
 Seq. ID LIB3431-054-P1-K1-G3
 Method BLASTX
 NCBI GI g3789954
 BLAST score 550
 E value 1.0e-56
 Match length 122
 % identity 93
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 402580
 Seq. ID LIB3431-054-P1-K1-G4
 Method BLASTX
 NCBI GI g1707657
 BLAST score 538
 E value 5.0e-55
 Match length 167
 % identity 62
 NCBI Description (Z71640) DnaJ homologue [Pisum sativum]

Seq. No. 402581
 Seq. ID LIB3431-054-P1-K1-G5
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 1.0e-19
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 402582
 Seq. ID LIB3431-054-P1-K1-G7
 Method BLASTX
 NCBI GI g729478
 BLAST score 794
 E value 5.0e-85
 Match length 153
 % identity 98
 NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
 >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+ reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_ (AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to a region of the predicted gene.; similar to ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

Seq. No.	402583
Seq. ID	LIB3431-054-P1-K1-H1
Method	BLASTX
NCBI GI	g3912968
BLAST score	172
E value	3.0e-12
Match length	123
% identity	30
NCBI Description	ALPHA-ADAPTIN HOMOLOG >gi_1890329_emb_CAA71991_ (Y11104) alpha-adaptin [Drosophila melanogaster]
Seq. No.	402584
Seq. ID	LIB3431-054-P1-K1-H11
Method	BLASTX
NCBI GI	g629670
BLAST score	348
E value	6.0e-33
Match length	94
% identity	68
NCBI Description	hypothetical protein - tomato
Seq. No.	402585
Seq. ID	LIB3431-054-P1-K1-H3
Method	BLASTX
NCBI GI	g3885894
BLAST score	398
E value	7.0e-39
Match length	90
% identity	87
NCBI Description	(AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
Seq. No.	402586
Seq. ID	LIB3431-054-P1-K1-H6
Method	BLASTX
NCBI GI	g22380
BLAST score	512
E value	6.0e-52
Match length	127
% identity	80
NCBI Description	(X59714) CAAT-box DNA binding protein subunit B (NF-YB) [Zea mays]
Seq. No.	402587
Seq. ID	LIB3431-054-P1-K1-H7
Method	BLASTX
NCBI GI	g320618
BLAST score	335
E value	3.0e-32
Match length	88
% identity	83
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf_1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No. 402588
 Seq. ID LIB3431-054-P1-K1-H9
 Method BLASTX
 NCBI GI g132105
 BLAST score 635
 E value 1.0e-66
 Match length 116
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 402589
 Seq. ID LIB3431-054-P1-N1-A10
 Method BLASTX
 NCBI GI g3913426
 BLAST score 300
 E value 2.0e-33
 Match length 118
 % identity 69
 NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) (SAMDC) >gi_1532048_emb_CAA69074_ (Y07766) S-adenosylmethionine decarboxylase [Oryza sativa]

Seq. No. 402590
 Seq. ID LIB3431-054-P1-N1-A3
 Method BLASTX
 NCBI GI g1173347
 BLAST score 276
 E value 1.0e-48
 Match length 116
 % identity 77
 NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]

Seq. No. 402591
 Seq. ID LIB3431-054-P1-N1-A5
 Method BLASTX
 NCBI GI g6093830
 BLAST score 155
 E value 4.0e-10
 Match length 37
 % identity 81
 NCBI Description PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME) [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II PROTEIN PSBY-2] >gi_3337435 (AF060198) PsbY precursor; putative photosystem II peptide [Spinacia oleracea]


```
Seq. No.      402602
Seq. ID       LIB3431-054-P1-N1-B6
Method        BLASTX
NCBI GI       g2696804
BLAST score   333
E value       3.0e-52
Match length  117
% identity    92
NCBI Description (AB009665) water channel protein [Oryza sativa]
```

```
Seq. No.      402603
Seq. ID      LIB3431-054-P1-N1-B8
Method       BLASTX
NCBI GI      g2407279
BLAST score   315
E value      3.0e-30
Match length  69
% identity    93
NCBI Description (AF017362) aldolase [Oryza sativa]
```

```
Seq. No.      402604
Seq. ID      LIB3431-054-P1-N1-B9
Method       BLASTX
NCBI GI      g3789954
BLAST score   328
E value      2.0e-30
Match length  63
% identity    95
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]
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```
Seq. No.          402605
Seq. ID           LIB3431-054-P1-N1-C1
Method            BLASTX
NCBI GI           g132166
BLAST score       156
E value           2.0e-10
Match length      31
% identity        84
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE).
                  >gi_81660_pir_S04048 ribulose-bisphosphate carboxylase
                  activase precursor - Arabidopsis thaliana
                  >gi_16471_emb_CAA32429_(X14212) rubisco activase (AA 1 -
                  473) [Arabidopsis thaliana]
```

```
Seq. No.      402606
Seq. ID      LIB3431-054-P1-N1-C11
Method       BLASTX
NCBI GI      g2651310
BLAST score   163
E value      3.0e-11
Match length  69
% identity    45
NCBI Description (AC002336) putative PTR2-B peptide transporter [Arabidopsis thaliana]
```


BLAST score 525
 E value 2.0e-53
 Match length 111
 % identity 91
 NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 402618
 Seq. ID LIB3431-054-P1-N1-D5
 Method BLASTX
 NCBI GI g124226
 BLAST score 385
 E value 9.0e-59
 Match length 127
 % identity 92
 NCBI Description INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D)
 >gi_100278_pir_S21059 translation initiation factor
 eIF-5A.2 - curled-leaved tobacco >gi_19702_emb_CAA45104
 (X63542) eukaryotic initiation factor 5A (2) [Nicotiana
 plumbaginifolia]

Seq. No. 402619
 Seq. ID LIB3431-054-P1-N1-D8
 Method BLASTX
 NCBI GI g2191138
 BLAST score 241
 E value 1.0e-21
 Match length 92
 % identity 64
 NCBI Description (AF007269) A_IG002N01.18 gene product [Arabidopsis
 thaliana]

Seq. No. 402620
 Seq. ID LIB3431-054-P1-N1-E11
 Method BLASTX
 NCBI GI g6093830
 BLAST score 160
 E value 7.0e-11
 Match length 62
 % identity 31
 NCBI Description PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME)
 [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II
 PROTEIN PSBY-2] >gi_3337435 (AF060198) PsbY precursor;
 putative photosytem II peptide [Spinacia oleracea]

Seq. No. 402621
 Seq. ID LIB3431-054-P1-N1-E2
 Method BLASTN
 NCBI GI g3819352
 BLAST score 58
 E value 9.0e-24
 Match length 82
 % identity 93
 NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG0813.rev

Seq. No. 402622
 Seq. ID LIB3431-054-P1-N1-E3
 Method BLASTX

Method BLASTX
 NCBI GI g2072555
 BLAST score 222
 E value 6.0e-18
 Match length 41
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 402628
 Seq. ID LIB3431-054-P1-N1-F2
 Method BLASTX
 NCBI GI g132105
 BLAST score 396
 E value 1.0e-38
 Match length 74
 % identity 96
 NCBI Description RIBULOSE BIPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 402629
 Seq. ID LIB3431-054-P1-N1-F3
 Method BLASTX
 NCBI GI g115787
 BLAST score 332
 E value 6.0e-55
 Match length 115
 % identity 97
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
 protein 2R precursor - rice >gi_20182_emb_CAA32109
 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
 [Oryza sativa]

Seq. No. 402630
 Seq. ID LIB3431-054-P1-N1-F4
 Method BLASTX
 NCBI GI g606817
 BLAST score 182
 E value 3.0e-28
 Match length 69
 % identity 78
 NCBI Description (U08404) carbonic anhydrase [Oryza sativa]
 >gi_5917783_gb_AAD56038.1 AF182806_1 (AF182806) carbonic
 anhydrase 3 [Oryza sativa]

Seq. No. 402631
 Seq. ID LIB3431-054-P1-N1-F6
 Method BLASTX


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Seq. No.          402636
Seq. ID           LIB3431-054-P1-N1-G10
Method            BLASTX
NCBI GI           g2118307
BLAST score       166
E value           4.0e-24
Match length      91
% identity        55
NCBI Description   cysteine synthase (EC 4.2.99.8) 3A - Arabidopsis thaliana
                  >gi_804950_emb_CAA58893_(X84097) cysteine synthase
                  [Arabidopsis thaliana] >gi_1096196_prf__2111276A Ser(Ac)
                  thiol lyase [Arabidopsis thaliana]
```

```
Seq. No.      402637
Seq. ID      LIB3431-054-P1-N1-G5
Method       BLASTX
NCBI GI      g2072555
BLAST score   230
E value      7.0e-19
Match length  44
% identity   98
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
               >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
               protein [Oryza sativa]
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Seq. No.          402638
Seq. ID           LIB3431-054-P1-N1-G6
Method            BLASTX
NCBI GI           g6015059
BLAST score       320
E value           9.0e-51
Match length      104
% identity         97
NCBI Description   ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_2996096
                   (AF030517) translation elongation factor-1_alpha; EF-1
                   alpha [Oryza sativa]
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Seq. No.          402639
Seq. ID           LIB3431-054-P1-N1-G7
Method            BLASTX
NCBI GI           g729478
BLAST score       429
E value           1.0e-73
Match length      152
% identity        93
NCBI Description  FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
                  >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
                  reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_
                  (AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to
                  a region of the predicted gene.; similar to
                  ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

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Seq. No.      402640
Seq. ID       LIB3431-054-P1-N1-H3
Method        BLASTX
NCBI GI       g3885894
BLAST score   253
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Seq. No. 402645
 Seq. ID LIB3431-055-P1-N1-A1
 Method BLASTX
 NCBI GI g1644427
 BLAST score 248
 E value 3.0e-21
 Match length 59
 % identity 78
 NCBI Description (U74610) glyoxalase II [Arabidopsis thaliana]

Seq. No. 402646
 Seq. ID LIB3431-055-P1-N1-A11
 Method BLASTX
 NCBI GI g517500
 BLAST score 360
 E value 3.0e-34
 Match length 87
 % identity 80
 NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf_1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No. 402647
 Seq. ID LIB3431-055-P1-N1-A2
 Method BLASTX
 NCBI GI g131225
 BLAST score 216
 E value 2.0e-17
 Match length 56
 % identity 73
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 402648
 Seq. ID LIB3431-055-P1-N1-A6
 Method BLASTX
 NCBI GI g693920
 BLAST score 414
 E value 2.0e-40
 Match length 80
 % identity 97
 NCBI Description (U21113) chlorophyll a/b binding protein [Solanum tuberosum]

Seq. No. 402649
 Seq. ID LIB3431-055-P1-N1-A7
 Method BLASTX
 NCBI GI g21699
 BLAST score 317
 E value 3.0e-29
 Match length 71
 % identity 83
 NCBI Description (X66013) cathepsin B [Triticum aestivum]

Seq. No. 402650

Match length 101
 % identity 85
 NCBI Description catalase (EC 1.11.1.6) catA - rice
 >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]

Seq. No. 402671
 Seq. ID LIB3431-055-P1-N1-E2
 Method BLASTN
 NCBI GI g3789951
 BLAST score 403
 E value 0.0e+00
 Match length 480
 % identity 96
 NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor
 (Cab27) mRNA, nuclear gene encoding chloroplast protein,
 complete cds

Seq. No. 402672
 Seq. ID LIB3431-055-P1-N1-E3
 Method BLASTX
 NCBI GI g4507769
 BLAST score 257
 E value 7.0e-37
 Match length 98
 % identity 74
 NCBI Description ubiquitin-conjugating enzyme E2A (RAD6 homolog)
 >gi_1351346_sp_P49459_UBCA HUMAN UBIQUITIN-CONJUGATING
 ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN
 CARRIER PROTEIN) (HR6A) >gi_108016_pir_A41222
 ubiquitin-conjugating enzyme HHR6A - human >gi_184044
 (M74524) HHR6A (Human homologue of yeast RAD 6); putative
 [Homo sapiens]

Seq. No. 402673
 Seq. ID LIB3431-055-P1-N1-E9
 Method BLASTX
 NCBI GI g4335763
 BLAST score 333
 E value 6.0e-31
 Match length 122
 % identity 55
 NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]

Seq. No. 402674
 Seq. ID LIB3431-055-P1-N1-F10
 Method BLASTX
 NCBI GI g4337175
 BLAST score 168
 E value 5.0e-25
 Match length 114
 % identity 58
 NCBI Description (AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906,
 gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
 gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and
 gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No. 402675

09684016-101000

Seq. ID LIB3431-055-P1-N1-F2
 Method BLASTX
 NCBI GI g115787
 BLAST score 362
 E value 3.0e-50
 Match length 107
 % identity 98
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 402676
 Seq. ID LIB3431-055-P1-N1-F3
 Method BLASTX
 NCBI GI g2407279
 BLAST score 211
 E value 2.0e-26
 Match length 66
 % identity 98
 NCBI Description (AF017362) aldolase [Oryza sativa]

Seq. No. 402677
 Seq. ID LIB3431-055-P1-N1-F5
 Method BLASTX
 NCBI GI g1321661
 BLAST score 427
 E value 5.0e-42
 Match length 83
 % identity 98
 NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]

Seq. No. 402678
 Seq. ID LIB3431-055-P1-N1-F6
 Method BLASTX
 NCBI GI g3036951
 BLAST score 343
 E value 2.0e-61
 Match length 122
 % identity 98
 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 402679
 Seq. ID LIB3431-055-P1-N1-F8
 Method BLASTN
 NCBI GI g2624325
 BLAST score 227
 E value 1.0e-124
 Match length 239
 % identity 99
 NCBI Description Oryza sativa mRNA for glycine-rich RNA-binding protein (OsGRP1)

Seq. No. 402680
 Seq. ID LIB3431-055-P1-N1-F9

% identity 98
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 402686
Seq. ID LIB3431-055-P1-N1-G5
Method BLASTX
NCBI GI g1617197
BLAST score 261
E value 2.0e-22
Match length 71
% identity 66
NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 402687
Seq. ID LIB3431-055-P1-N1-G6
Method BLASTX
NCBI GI g131225
BLAST score 309
E value 3.0e-28
Match length 75
% identity 79
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 402688
Seq. ID LIB3431-055-P1-N1-G8
Method BLASTX
NCBI GI g1076724
BLAST score 233
E value 1.0e-31
Match length 77
% identity 88
NCBI Description LHCI-680, photosystem I antenna protein - barley >gi_666054_emb_CAA59049 (X84308) LHCI-680, photosystem I antenna protein [Hordeum vulgare]

Seq. No. 402689
Seq. ID LIB3431-055-P1-N1-G9
Method BLASTX
NCBI GI g1617197
BLAST score 204
E value 7.0e-16
Match length 47
% identity 79
NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 402690
Seq. ID LIB3431-055-P1-N1-H1
Method BLASTN
NCBI GI g3063523
BLAST score 117
E value 4.0e-59
Match length 281
% identity 86
NCBI Description Oryza sativa ribulose 1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 402691
 Seq. ID LIB3431-055-P1-N1-H11
 Method BLASTX
 NCBI GI g3004565
 BLAST score 255
 E value 9.0e-22
 Match length 94
 % identity 55
 NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 402692
 Seq. ID LIB3431-055-P1-N1-H2
 Method BLASTN
 NCBI GI g2773153
 BLAST score 371
 E value 0.0e+00
 Match length 375
 % identity 100
 NCBI Description Oryza sativa abscisic acid- and stress-inducible protein (Asr1) mRNA, complete cds

Seq. No. 402693
 Seq. ID LIB3431-055-P1-N1-H3
 Method BLASTX
 NCBI GI g548605
 BLAST score 420
 E value 4.0e-56
 Match length 131
 % identity 91
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir_A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No. 402694
 Seq. ID LIB3431-055-P1-N1-H4
 Method BLASTX
 NCBI GI g115813
 BLAST score 432
 E value 1.0e-42
 Match length 104
 % identity 81
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 402695
 Seq. ID LIB3431-055-P1-N1-H5
 Method BLASTX
 NCBI GI g132105
 BLAST score 521
 E value 6.0e-53
 Match length 99
 % identity 97

E value 7.0e-34
 Match length 90
 % identity 90
 NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_1816586
 (U85494) LON1 protease [Zea mays]

Seq. No. 402706
 Seq. ID LIB3431-055-P2-K1-C1
 Method BLASTX
 NCBI GI g3126854
 BLAST score 443
 E value 5.0e-44
 Match length 119
 % identity 84
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 402707
 Seq. ID LIB3431-055-P2-K1-C11
 Method BLASTN
 NCBI GI g3885885
 BLAST score 32
 E value 3.0e-09
 Match length 32
 % identity 100
 NCBI Description Oryza sativa Rieske Fe-S precursor protein (RISP) mRNA,
 complete cds

Seq. No. 402708
 Seq. ID LIB3431-055-P2-K1-C6
 Method BLASTN
 NCBI GI g303856
 BLAST score 139
 E value 4.0e-72
 Match length 227
 % identity 93
 NCBI Description Rice mRNA for ubiquitin protein fused to a ribosomal
 protein, complete cds

Seq. No. 402709
 Seq. ID LIB3431-055-P2-K1-C7
 Method BLASTX
 NCBI GI g517500
 BLAST score 160
 E value 1.0e-10
 Match length 61
 % identity 57
 NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa
 protein [Zea mays] >gi_444338_prf__1906386A photosystem II
 OE17 protein [Pisum sativum]

Seq. No. 402710
 Seq. ID LIB3431-055-P2-K1-D11
 Method BLASTN
 NCBI GI g6016845
 BLAST score 66
 E value 1.0e-28
 Match length 108

Seq. ID LIB3431-055-P2-K1-F9
 Method BLASTX
 NCBI GI g2407281
 BLAST score 645
 E value 1.0e-67
 Match length 122
 % identity 97
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 402717
 Seq. ID LIB3431-055-P2-K1-G10
 Method BLASTN
 NCBI GI g3075487
 BLAST score 99
 E value 1.0e-48
 Match length 123
 % identity 95
 NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No. 402718
 Seq. ID LIB3431-055-P2-K1-G2
 Method BLASTN
 NCBI GI g20262
 BLAST score 227
 E value 1.0e-125
 Match length 231
 % identity 100
 NCBI Description O.sativa light-induced mRNA

Seq. No. 402719
 Seq. ID LIB3431-055-P2-K1-H11
 Method BLASTX
 NCBI GI g3004565
 BLAST score 340
 E value 4.0e-32
 Match length 97
 % identity 66
 NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 402720
 Seq. ID LIB3431-055-P2-K1-H12
 Method BLASTX
 NCBI GI g4678920
 BLAST score 227
 E value 1.0e-18
 Match length 102
 % identity 48
 NCBI Description (AL049711) putative heat shock transcription factor [Arabidopsis thaliana]

Seq. No. 402721
 Seq. ID LIB3431-055-P2-K1-H2
 Method BLASTN
 NCBI GI g2773153
 BLAST score 171

E value 2.0e-91
 Match length 186
 % identity 98
 NCBI Description Oryza sativa abscisic acid- and stress-inducible protein (Asr1) mRNA, complete cds

Seq. No. 402722
 Seq. ID LIB3431-055-P2-K1-H6
 Method BLASTX
 NCBI GI g2407281
 BLAST score 575
 E value 2.0e-59
 Match length 113
 % identity 96
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 402723
 Seq. ID LIB3431-055-P2-K1-H7
 Method BLASTX
 NCBI GI g3808101
 BLAST score 211
 E value 2.0e-26
 Match length 95
 % identity 74
 NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]

Seq. No. 402724
 Seq. ID LIB3431-055-P2-K1-H8
 Method BLASTN
 NCBI GI g2570512
 BLAST score 51
 E value 2.0e-20
 Match length 55
 % identity 98
 NCBI Description Oryza sativa chlorophyll a-b binding protein mRNA, complete cds

Seq. No. 402725
 Seq. ID LIB3431-056-P1-K1-A1
 Method BLASTX
 NCBI GI g5690431
 BLAST score 241
 E value 2.0e-20
 Match length 97
 % identity 48
 NCBI Description (AF165883) prefoldin subunit 2 [Homo sapiens]

Seq. No. 402726
 Seq. ID LIB3431-056-P1-K1-A10
 Method BLASTX
 NCBI GI g132105
 BLAST score 609
 E value 2.0e-63
 Match length 131
 % identity 88
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 402727
 Seq. ID LIB3431-056-P1-K1-A11
 Method BLASTX
 NCBI GI g1519251
 BLAST score 673
 E value 7.0e-71
 Match length 150
 % identity 91
 NCBI Description (U65957) GF14-c protein [Oryza sativa]

Seq. No. 402728
 Seq. ID LIB3431-056-P1-K1-A2
 Method BLASTX
 NCBI GI g3126854
 BLAST score 488
 E value 3.0e-49
 Match length 114
 % identity 85
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 402729
 Seq. ID LIB3431-056-P1-K1-A3
 Method BLASTN
 NCBI GI g4959460
 BLAST score 36
 E value 1.0e-10
 Match length 36
 % identity 100
 NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No. 402730
 Seq. ID LIB3431-056-P1-K1-A4
 Method BLASTN
 NCBI GI g4959460
 BLAST score 35
 E value 6.0e-10
 Match length 35
 % identity 100
 NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No. 402731
 Seq. ID LIB3431-056-P1-K1-A5
 Method BLASTX
 NCBI GI g5734634
 BLAST score 318
 E value 3.0e-29
 Match length 107
 % identity 53

NCBI Description (AP000391) Similar to putative lipase (AC006232) [Oryza sativa]

Seq. No. 402732
 Seq. ID LIB3431-056-P1-K1-A6
 Method BLASTX
 NCBI GI g3288821
 BLAST score 259
 E value 2.0e-47
 Match length 110
 % identity 87

NCBI Description (AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana]
 >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209)
 alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

Seq. No. 402733
 Seq. ID LIB3431-056-P1-K1-A8
 Method BLASTN
 NCBI GI g1245938
 BLAST score 35
 E value 5.0e-10
 Match length 35
 % identity 100

NCBI Description rabClC-2 beta=chloride channel ClC-2G isoform [rabbits, heart atrium, mRNA, 2998 nt]

Seq. No. 402734
 Seq. ID LIB3431-056-P1-K1-B1
 Method BLASTX
 NCBI GI g132096
 BLAST score 500
 E value 8.0e-60
 Match length 125
 % identity 94

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN A PRECURSOR (RUBISCO SMALL SUBUNIT A) >gi_68095_pir_RKRZS6
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS2106) - rice >gi_218210_dbj_BAA00539_ (D00644) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa]

Seq. No. 402735
 Seq. ID LIB3431-056-P1-K1-B10
 Method BLASTX
 NCBI GI g4678311
 BLAST score 272
 E value 6.0e-24
 Match length 77
 % identity 68

NCBI Description (AL049655) aquaporin/MIP-like protein [Arabidopsis thaliana]

Seq. No. 402736
 Seq. ID LIB3431-056-P1-K1-B11
 Method BLASTX
 NCBI GI g1076724

BLAST score 451
E value 4.0e-66
Match length 141
% identity 87
NCBI Description LHCI-680, photosystem I antenna protein - barley
>gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
antenna protein [Hordeum vulgare]

Seq. No. 402737
Seq. ID LIB3431-056-P1-K1-B12
Method BLASTX
NCBI GI g3789952
BLAST score 652
E value 2.0e-68
Match length 132
% identity 96
NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza
sativa]

Seq. No. 402738
Seq. ID LIB3431-056-P1-K1-B2
Method BLASTN
NCBI GI g433216
BLAST score 115
E value 6.0e-58
Match length 118
% identity 99
NCBI Description Rice mRNA for ascorbate peroxidase (gene name SS622),
partial cds

Seq. No. 402739
Seq. ID LIB3431-056-P1-K1-B4
Method BLASTX
NCBI GI g1173347
BLAST score 326
E value 2.0e-39
Match length 103
% identity 87
NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
>gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC
3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
(X65540) sedoheptulose-1,7-bisphosphatase [Triticum
aestivum]

Seq. No. 402740
Seq. ID LIB3431-056-P1-K1-B6
Method BLASTX
NCBI GI g2407281
BLAST score 673
E value 6.0e-71
Match length 133
% identity 94
NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
subunit [Oryza sativa]

Seq. No. 402741

NCBI GI g132105
 BLAST score 537
 E value 6.0e-55
 Match length 111
 % identity 91
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 402747
 Seq. ID LIB3431-056-P1-K1-C2
 Method BLASTX
 NCBI GI g2073375
 BLAST score 459
 E value 2.0e-54
 Match length 110
 % identity 90
 NCBI Description (D85317) farnesyl pyrophosphate synthase [Oryza sativa] >gi_4063829_dbj_BAA36276_ (AB021747) farnesyl diphosphate synthase [Oryza sativa]

Seq. No. 402748
 Seq. ID LIB3431-056-P1-K1-C3
 Method BLASTX
 NCBI GI g417260
 BLAST score 421
 E value 3.0e-41
 Match length 128
 % identity 66
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]

Seq. No. 402749
 Seq. ID LIB3431-056-P1-K1-C4
 Method BLASTX
 NCBI GI g2407281
 BLAST score 650
 E value 3.0e-68
 Match length 125
 % identity 94
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 402750
 Seq. ID LIB3431-056-P1-K1-C5
 Method BLASTX
 NCBI GI g2191151
 BLAST score 170
 E value 4.0e-17
 Match length 87

% identity 60
 NCBI Description (AF007269) contains similarity to membrane associated salt-inducible protein [Arabidopsis thaliana]

Seq. No. 402751
 Seq. ID LIB3431-056-P1-K1-C6
 Method BLASTX
 NCBI GI g548605
 BLAST score 541
 E value 2.0e-55
 Match length 118
 % identity 91
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
 >gi_539055_pir_A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No. 402752
 Seq. ID LIB3431-056-P1-K1-C7
 Method BLASTX
 NCBI GI g871931
 BLAST score 416
 E value 1.0e-40
 Match length 108
 % identity 78
 NCBI Description (D30763) ferredoxin [Oryza sativa]

Seq. No. 402753
 Seq. ID LIB3431-056-P1-K1-C9
 Method BLASTX
 NCBI GI g2688828
 BLAST score 169
 E value 7.0e-12
 Match length 82
 % identity 43
 NCBI Description (U97530) ethylene-forming-enzyme-like dioxygenase [Prunus armeniaca]

Seq. No. 402754
 Seq. ID LIB3431-056-P1-K1-D1
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 402755
 Seq. ID LIB3431-056-P1-K1-D12
 Method BLASTX
 NCBI GI g671740
 BLAST score 606
 E value 5.0e-63

Match length 111
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 402756
 Seq. ID LIB3431-056-P1-K1-D3
 Method BLASTX
 NCBI GI g1076660
 BLAST score 219
 E value 9.0e-20
 Match length 126
 % identity 45
 NCBI Description D13F(MYBST1) protein - potato >gi_786426_bbs_159122 (S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes, leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. No. 402757
 Seq. ID LIB3431-056-P1-K1-D4
 Method BLASTN
 NCBI GI g6015437
 BLAST score 36
 E value 9.0e-11
 Match length 36
 % identity 100
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 402758
 Seq. ID LIB3431-056-P1-K1-D5
 Method BLASTN
 NCBI GI g218209
 BLAST score 135
 E value 9.0e-70
 Match length 246
 % identity 93
 NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No. 402759
 Seq. ID LIB3431-056-P1-K1-D6
 Method BLASTX
 NCBI GI g3738261
 BLAST score 209
 E value 9.0e-17
 Match length 48
 % identity 92
 NCBI Description (AB018412) chloroplast phosphoglycerate kinase [Populus nigra]

Seq. No. 402760
 Seq. ID LIB3431-056-P1-K1-D7
 Method BLASTX
 NCBI GI g320618
 BLAST score 648
 E value 6.0e-68


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BLAST score          581
E value              4.0e-60
Match length         121
% identity            86
NCBI Description     LHCI-680, photosystem I antenna protein - barley
                    >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                    antenna protein [Hordeum vulgare]

Seq. No.             402766
Seq. ID              LIB3431-056-P1-K1-E12
Method               BLASTX
NCBI GI              g1084461
BLAST score          212
E value              5.0e-17
Match length         79
% identity            56
NCBI Description     RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]

Seq. No.             402767
Seq. ID              LIB3431-056-P1-K1-E2
Method               BLASTX
NCBI GI              g82080
BLAST score          336
E value              1.0e-32
Match length         113
% identity            68
NCBI Description     chlorophyll a/b-binding protein type III precursor - tomato
                    >gi_226872_prf_1609235A chlorophyll a/b binding protein
                    [Lycopersicon esculentum]

Seq. No.             402768
Seq. ID              LIB3431-056-P1-K1-E4
Method               BLASTN
NCBI GI              g6015437
BLAST score          38
E value              5.0e-12
Match length         38
% identity            100
NCBI Description     Homo sapiens PEX1 mRNA, complete cds

Seq. No.             402769
Seq. ID              LIB3431-056-P1-K1-E7
Method               BLASTX
NCBI GI              g5733872
BLAST score          457
E value              2.0e-45
Match length         119
% identity            74
NCBI Description     (AC007932) Similar to gi_4982048 ribosomal protein L18 from
                    Thermotoga maritima genome gb AE001798. ESTs gb_Z35613,
                    gb_T75951, gb_T22182, gb_T45962, gb_H76281 and gb_AI100025
                    come from this gene. [Arabidopsis thaliana]

Seq. No.             402770
Seq. ID              LIB3431-056-P1-K1-E9
Method               BLASTX
NCBI GI              q3789952

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BLAST score      235
E value         2.0e-19
Match length    44
% identity      100
NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza
sativa]
```

```
Seq. No.          402771
Seq. ID           LIB3431-056-P1-K1-F1
Method            BLASTX
NCBI GI           g115787
BLAST score       636
E value           2.0e-74
Match length      142
% identity        95
NCBI Description   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
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Seq. No.      402772
Seq. ID       LIB3431-056-P1-K1-F10
Method        BLASTX
NCBI GI       g1173347
BLAST score   605
E value       4.0e-63
Match length  117
% identity    95
NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC
                3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                aestivum]
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Seq. No.          402773
Seq. ID           LIB3431-056-P1-K1-F12,
Method            BLASTX
NCBI GI           g3913808
BLAST score       477
E value           6.0e-48
Match length      102
% identity        88
NCBI Description  FERROCHELATASE PRECURSOR (PROTOHEME FERRO-LYASE) (HEME
                  SYNTHETASE) >gi_2429618_dbj_BAA22284_ (AB007120)
                  ferrochelatase [Oryza sativa]
```

```
Seq. No.          402774
Seq. ID           LIB3431-056-P1-K1-F2
Method            BLASTX
NCBI GI           g585350
BLAST score       384
E value           3.0e-37
Match length      109
% identity        68
NCBI Description   CASEIN KINASE II, ALPHA CHAIN 2 (CK II)
```

0904016 12 103000

```
Seq. No.      402776
Seq. ID      LIB3431-056-P1-K1-F5
Method       BLASTX
NCBI GI      g2506826
BLAST score   328
E value      2.0e-30
Match length  90
% identity    74
NCBI Description  NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
(PAPI) >gi_1619604_emb_CAA69949.1_ (Y08691) lipid transfer
protein [Oryza sativa] >gi_1667590_ (U77295) lipid transfer
protein [Oryza sativa]
```

```
Seq. No. 402778
Seq. ID LIB3431-056-P1-K1-F7
Method BLASTN
NCBI GI g2062705
BLAST score 37
E value 3.0e-11
Match length 37
% identity 100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
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51759

BLAST score 430
E value 2.0e-42
Match length 138
% identity 58
NCBI Description (AC007369) Putative RNA helicase [Arabidopsis thaliana]

Seq. No. 402780
Seq. ID LIB3431-056-P1-K1-G1
Method BLASTX
NCBI GI g3335349
BLAST score 416
E value 1.0e-40
Match length 155
% identity 54
NCBI Description (AC004512) Similar to gb_U46691 putative chromatin structure regulator (SUPT6H) from Homo sapiens. ESTs gb_T42908, gb_AA586170 and gb_AA395125 come from this gene. [Arabidopsis thaliana]

Seq. No. 402781
Seq. ID LIB3431-056-P1-K1-G10
Method BLASTX
NCBI GI g5326825
BLAST score 164
E value 3.0e-11
Match length 90
% identity 32
NCBI Description (AF044953) NADH:ubiquinone oxidoreductase PGIV subunit [Homo sapiens]

Seq. No. 402782
Seq. ID LIB3431-056-P1-K1-G12
Method BLASTX
NCBI GI g320618
BLAST score 512
E value 4.0e-52
Match length 114
% identity 85
NCBI Description chlorophyll a/b-binding protein I precursor - rice
>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa]
>gi_227611_prf_1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No. 402783
Seq. ID LIB3431-056-P1-K1-G2
Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 1.0e-19
Match length 44
% identity 100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 402784

09684016 101000

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Seq. No.      402800
Seq. ID      LIB3431-056-P1-N1-A11
Method       BLASTN
NCBI GI      g2331130
BLAST score   100
E value      8.0e-49
Match length  148
% identity    92
NCBI Description  Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds
```

```
Seq. No.      402801
Seq. ID      LIB3431-056-P1-N1-A12
Method       BLASTX
NCBI GI      g131225
BLAST score   203
E value      7.0e-16
Match length  71
% identity    58
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein
precursor - barley >gi_167087 (M61146) photosystem I
hydrophobic protein [Hordeum vulgare]
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Seq. No.          402802
Seq. ID           LIB3431-056-P1-N1-A2
Method            BLASTX
NCBI GI           g3126854
BLAST score       349
E value           9.0e-33
Match length      66
% identity        100
NCBI Description  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```

51764

Seq. No. 402813
 Seq. ID LIB3431-056-P1-N1-C1
 Method BLASTX
 NCBI GI g4079798
 BLAST score 414
 E value 2.0e-40
 Match length 81
 % identity 99
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 402814
 Seq. ID LIB3431-056-P1-N1-C10
 Method BLASTX
 NCBI GI g3885896
 BLAST score 524
 E value 2.0e-53
 Match length 100
 % identity 100
 NCBI Description (AF093636) plastocyanin precursor [Oryza sativa]

Seq. No. 402815
 Seq. ID LIB3431-056-P1-N1-C12
 Method BLASTN
 NCBI GI g218209
 BLAST score 37
 E value 3.0e-11
 Match length 53
 % identity 92
 NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No. 402816
 Seq. ID LIB3431-056-P1-N1-C2
 Method BLASTX
 NCBI GI g2073375
 BLAST score 576
 E value 2.0e-59
 Match length 107
 % identity 100
 NCBI Description (D85317) farnesyl pyrophosphate synthase [Oryza sativa]
 >gi_4063829_dbj_BAA36276_ (AB021747) farnesyl diphosphate synthase [Oryza sativa]

Seq. No. 402817
 Seq. ID LIB3431-056-P1-N1-C3
 Method BLASTX
 NCBI GI g417260
 BLAST score 321
 E value 1.0e-29
 Match length 106
 % identity 61
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

```
Seq. No.          402818
Seq. ID           LIB3431-056-P1-N1-C4
Method            BLASTX
NCBI GI           g671740
BLAST score       361
E value           3.0e-34
Match length      70
% identity        97
NCBI Description   (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
```

```
Seq. No.          402819
Seq. ID           LIB3431-056-P1-N1-C6
Method            BLASTX
NCBI GI           g548605
BLAST score       599
E value           5.0e-62
Match length      131
% identity        91
NCBI Description  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi_539055_pir_A48527 photosystem I protein psaK precursor
                  - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
```

```
Seq. No.          402820
Seq. ID           LIB3431-056-P1-N1-C7
Method            BLASTX
NCBI GI           g871931
BLAST score       161
E value           5.0e-11
Match length      44
% identity        75
NCBI Description   (D30763) ferredoxin [Oryza sativa]
```

```
Seq. No.      402821
Seq. ID      LIB3431-056-P1-N1-D1
Method       BLASTX
NCBI GI      g2072555
BLAST score   228
E value      1.0e-18
Match length  42
% identity    100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
                >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                protein [Oryza sativa]
```

```
Seq. No.      402822
Seq. ID       LIB3431-056-P1-N1-D12
Method        BLASTX
NCBI GI       g671740
BLAST score   433
E value       1.0e-42
Match length  78
% identity    100
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
construct]
```

Seq. No. 402823
 Seq. ID LIB3431-056-P1-N1-D3
 Method BLASTX
 NCBI GI g1076660
 BLAST score 222
 E value 6.0e-18
 Match length 89
 % identity 57
 NCBI Description D13F(MYBST1) protein - potato >gi_786426_bbs_159122
 (S74753) MybSt1=Myb-related transcriptional activator
 {DNA-binding domain repeats} [Solanum tuberosum=potatoes,
 leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. No. 402824
 Seq. ID LIB3431-056-P1-N1-D5
 Method BLASTN
 NCBI GI g218209
 BLAST score 39
 E value 2.0e-12
 Match length 55
 % identity 93
 NCBI Description Oryza sativa mRNA for the small subunit of
 ribulose-1,5-bisphosphate carboxylase, complete cds, clone
 POSSS2106

Seq. No. 402825
 Seq. ID LIB3431-056-P1-N1-D7
 Method BLASTX
 NCBI GI g115787
 BLAST score 409
 E value 6.0e-40
 Match length 77
 % identity 100
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
 protein 2R precursor - rice >gi_20182_emb_CAA32109
 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
 [Oryza sativa]

Seq. No. 402826
 Seq. ID LIB3431-056-P1-N1-D8
 Method BLASTX
 NCBI GI g3885892
 BLAST score 544
 E value 9.0e-56
 Match length 102
 % identity 100
 NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 402827
 Seq. ID LIB3431-056-P1-N1-D9
 Method BLASTX
 NCBI GI g3885892
 BLAST score 286
 E value 2.0e-25
 Match length 57

% identity 100
NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 402828
Seq. ID LIB3431-056-P1-N1-E1
Method BLASTX
NCBI GI g3789954
BLAST score 611
E value 2.0e-63
Match length 113
% identity 100
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 402829
Seq. ID LIB3431-056-P1-N1-E11
Method BLASTX
NCBI GI g1076724
BLAST score 374
E value 8.0e-36
Match length 72
% identity 94
NCBI Description LHCI-680, photosystem I antenna protein - barley
>gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
antenna protein [Hordeum vulgare]

Seq. No. 402830
Seq. ID LIB3431-056-P1-N1-E12
Method BLASTX
NCBI GI g1084461
BLAST score 287
E value 1.0e-25
Match length 98
% identity 60
NCBI Description RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]

Seq. No. 402831
Seq. ID LIB3431-056-P1-N1-E2
Method BLASTX
NCBI GI g115813
BLAST score 234
E value 2.0e-19
Match length 56
% identity 80
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 402832
Seq. ID LIB3431-056-P1-N1-E7
Method BLASTX
NCBI GI g5733872
BLAST score 182
E value 2.0e-13
Match length 57
% identity 60
NCBI Description (AC007932) Similar to gi_4982048 ribosomal protein L18 from

060941

```
Seq. No.          402836
Seq. ID          LIB3431-056-P1-N1-F10
Method           BLASTX
NCBI GI          g1173347
BLAST score       401
E value          6.0e-39
Match length      85
% identity        96
NCBI Description  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                  (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                  (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
```

Seq. No. 402837
 Seq. ID LIB3431-056-P1-N1-F11
 Method BLASTX
 NCBI GI g2244734
 BLAST score 166
 E value 2.0e-11
 Match length 32
 % identity 97
 NCBI Description (D88414) actin [*Gossypium hirsutum*]

Seq. No. 402838
 Seq. ID LIB3431-056-P1-N1-F2
 Method BLASTX
 NCBI GI g585350
 BLAST score 496
 E value 5.0e-50
 Match length 110
 % identity 83
 NCBI Description CASEIN KINASE II, ALPHA CHAIN 2 (CK II)
 >gi_419753_pir_S31099 casein kinase II (EC 2.7.1.-)
 alpha-type chain (clone ATCKA2) - *Arabidopsis thaliana*
 >gi_391605_dbj_BAA01091 (D10247) casein kinase II
 catalytic subunit [*Arabidopsis thaliana*]

Seq. No. 402839
 Seq. ID LIB3431-056-P1-N1-F3
 Method BLASTX
 NCBI GI g3036951
 BLAST score 427
 E value 6.0e-42
 Match length 80
 % identity 100
 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein
 [*Nicotiana sylvestris*]

Seq. No. 402840
 Seq. ID LIB3431-056-P1-N1-F5
 Method BLASTN
 NCBI GI g1619603
 BLAST score 370
 E value 0.0e+00
 Match length 414
 % identity 97
 NCBI Description O.sativa mRNA for lipid transfer protein
 >gi_1667589_gb_U77295_OSU77295 *Oryza sativa* lipid transfer
 protein (LTP) mRNA, complete cds

Seq. No. 402841
 Seq. ID LIB3431-056-P1-N1-F9
 Method BLASTX
 NCBI GI g2673917
 BLAST score 305
 E value 1.0e-27
 Match length 80
 % identity 66
 NCBI Description (AC002561) putative ATP-dependent RNA helicase [*Arabidopsis*]

09690-10100

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Seq. No.          402846
Seq. ID           LIB3431-056-P1-N1-G2
Method            BLASTX
NCBI GI           g2072555
BLAST score       228
E value           1.0e-18
Match length      42
% identity        100
```

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
protein [Oryza sativa]

Seq. No. 402847
Seq. ID LIB3431-056-P1-N1-G3
Method BLASTX
NCBI GI g115787
BLAST score 676
E value 4.0e-71
Match length 130
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
protein 2R precursor - rice >gi_20182_emb_CAA32109
(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
[Oryza sativa]

Seq. No. 402848
Seq. ID LIB3431-056-P1-N1-G4
Method BLASTX
NCBI GI g3036951
BLAST score 650
E value 4.0e-68
Match length 124
% identity 98

NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein
[Nicotiana sylvestris]

Seq. No. 402849
Seq. ID LIB3431-056-P1-N1-G5
Method BLASTX
NCBI GI g548605
BLAST score 301
E value 2.0e-27
Match length 64
% identity 92

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
>gi_539055_pir_A48527 photosystem I protein psaK precursor
- barley >gi_304220 (L12707) photosystem I PSI-K subunit
[Hordeum vulgare]

Seq. No. 402850
Seq. ID LIB3431-056-P1-N1-G6
Method BLASTX
NCBI GI g417154
BLAST score 392
E value 7.0e-38
Match length 93
% identity 85

NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir_S25541 heat shock
protein 82 - rice (strain Taichung Native One)
>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
(HSP82) [Oryza sativa]

Seq. No. 402851

Seq. ID LIB3431-056-P1-N1-G9
Method BLASTX
NCBI GI g4006881
BLAST score 585
E value 2.0e-60
Match length 139
% identity 79
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 402852
Seq. ID LIB3431-056-P1-N1-H1
Method BLASTN
NCBI GI g3345476
BLAST score 342
E value 0.0e+00
Match length 386
% identity 97
NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds

Seq. No. 402853
Seq. ID LIB3431-056-P1-N1-H2
Method BLASTN
NCBI GI g22469
BLAST score 34
E value 1.0e-09
Match length 38
% identity 97
NCBI Description Maize mRNA for cytoplasmic ribosomal protein S11

Seq. No. 402854
Seq. ID LIB3431-056-P1-N1-H5
Method BLASTN
NCBI GI g14264
BLAST score 67
E value 3.0e-29
Match length 115
% identity 90
NCBI Description T.aestivum gene for sedoheptulose-1,7-bisphosphatase

Seq. No. 402855
Seq. ID LIB3431-056-P1-N1-H9
Method BLASTX
NCBI GI g671740
BLAST score 546
E value 6.0e-56
Match length 99
% identity 100
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 402856
Seq. ID LIB3431-058-P1-K1-A1
Method BLASTX
NCBI GI g3355468
BLAST score 355
E value 1.0e-33
Match length 96

% identity 85
 NCBI Description (AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No. 402857
 Seq. ID LIB3431-058-P1-K1-A10
 Method BLASTX
 NCBI GI g2244749
 BLAST score 383
 E value 7.0e-37
 Match length 112
 % identity 66
 NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No. 402858
 Seq. ID LIB3431-058-P1-K1-A12
 Method BLASTX
 NCBI GI g3345477
 BLAST score 214
 E value 4.0e-17
 Match length 41
 % identity 95
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 402859
 Seq. ID LIB3431-058-P1-K1-A2
 Method BLASTX
 NCBI GI g1514643
 BLAST score 180
 E value 4.0e-26
 Match length 102
 % identity 63
 NCBI Description (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]

Seq. No. 402860
 Seq. ID LIB3431-058-P1-K1-A3
 Method BLASTN
 NCBI GI g1159878
 BLAST score 52
 E value 3.0e-20
 Match length 64
 % identity 95
 NCBI Description A.fatua mRNA for DNA-binding protein (clone ABF2)

Seq. No. 402861
 Seq. ID LIB3431-058-P1-K1-A4
 Method BLASTX
 NCBI GI g2072555
 BLAST score 165
 E value 3.0e-11
 Match length 32
 % identity 94
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 402862

Seq. ID LIB3431-058-P1-K1-A5
 Method BLASTX
 NCBI GI g2462760
 BLAST score 143
 E value 8.0e-09
 Match length 75
 % identity 39
 NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 402863
 Seq. ID LIB3431-058-P1-K1-A6
 Method BLASTX
 NCBI GI g3402713
 BLAST score 379
 E value 2.0e-36
 Match length 123
 % identity 60
 NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No. 402864
 Seq. ID LIB3431-058-P1-K1-A7
 Method BLASTX
 NCBI GI g132105
 BLAST score 494
 E value 6.0e-50
 Match length 109
 % identity 83
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 402865
 Seq. ID LIB3431-058-P1-K1-A8
 Method BLASTX
 NCBI GI g3046693
 BLAST score 573
 E value 3.0e-59
 Match length 136
 % identity 74
 NCBI Description (AL022140) receptor like protein (fragment) [Arabidopsis thaliana]

Seq. No. 402866
 Seq. ID LIB3431-058-P1-K1-A9
 Method BLASTX
 NCBI GI g3550983
 BLAST score 358
 E value 5.0e-34
 Match length 98
 % identity 68
 NCBI Description (AB010690) mutM homologue-2 [Arabidopsis thaliana]

>gi_3820622 (AF099971) putative formamidopyrimidine-DNA glycosylase 2 [Arabidopsis thaliana]
 >gi_5903054_gb_AAD55613.1_AC008016_23 (AC008016) Identical to gb_AB010690 mutM homologue-2 (formamidopyrimidine-DNA glycosylase 1) from Arabidopsis thaliana. EST gb_Z18192 comes from this gene

Seq. No. 402867
 Seq. ID LIB3431-058-P1-K1-B10
 Method BLASTX
 NCBI GI g3885886
 BLAST score 748
 E value 1.0e-79
 Match length 144
 % identity 100
 NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]

Seq. No. 402868
 Seq. ID LIB3431-058-P1-K1-B11
 Method BLASTX
 NCBI GI g2582381
 BLAST score 458
 E value 4.0e-46
 Match length 87
 % identity 93
 NCBI Description (AF021220) cation-chloride co-transporter [Nicotiana tabacum]

Seq. No. 402869
 Seq. ID LIB3431-058-P1-K1-B12
 Method BLASTX
 NCBI GI g2570511
 BLAST score 485
 E value 5.0e-49
 Match length 92
 % identity 99
 NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No. 402870
 Seq. ID LIB3431-058-P1-K1-B2
 Method BLASTX
 NCBI GI g3850566
 BLAST score 236
 E value 1.0e-22
 Match length 156
 % identity 40
 NCBI Description (AC005278) F15K9.3 [Arabidopsis thaliana]

Seq. No. 402871
 Seq. ID LIB3431-058-P1-K1-B3
 Method BLASTN
 NCBI GI g5730046
 BLAST score 35
 E value 3.0e-10
 Match length 35
 % identity 100
 NCBI Description Homo sapiens solute carrier family 17 (sodium phosphate),

member 3 (SLC17A3) mRNA >gi_2062691_gb U90545 HSU90545
Human sodium phosphate transporter (NPT4) mRNA, complete
cds

Seq. No. 402872
Seq. ID LIB3431-058-P1-K1-B5
Method BLASTX
NCBI GI g430947
BLAST score 360
E value 3.0e-34
Match length 102
% identity 71
NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein
[Arabidopsis thaliana]

Seq. No. 402873
Seq. ID LIB3431-058-P1-K1-B6
Method BLASTX
NCBI GI g132105
BLAST score 468
E value 4.0e-52
Match length 101
% identity 100
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 402874
Seq. ID LIB3431-058-P1-K1-B7
Method BLASTX
NCBI GI g21839
BLAST score 734
E value 5.0e-78
Match length 148
% identity 93
NCBI Description (X57952) phosphoribulokinase [Triticum aestivum]

Seq. No. 402875
Seq. ID LIB3431-058-P1-K1-B8
Method BLASTX
NCBI GI g82080
BLAST score 152
E value 4.0e-10
Match length 68
% identity 51
NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
>gi_226872_prf_1609235A chlorophyll a/b binding protein
[Lycopersicon esculentum]

Seq. No. 402876
Seq. ID LIB3431-058-P1-K1-B9

Method BLASTX
 NCBI GI g671740
 BLAST score 588
 E value 5.0e-61
 Match length 108
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 402877
 Seq. ID LIB3431-058-P1-K1-C1
 Method BLASTX
 NCBI GI g2191138
 BLAST score 310
 E value 3.0e-28
 Match length 136
 % identity 53
 NCBI Description (AF007269) A_IG002N01.18 gene product [Arabidopsis thaliana]

Seq. No. 402878
 Seq. ID LIB3431-058-P1-K1-C10
 Method BLASTX
 NCBI GI g1001355
 BLAST score 228
 E value 7.0e-19
 Match length 119
 % identity 42
 NCBI Description (D64006) auxin-induced protein [Synechocystis sp.]

Seq. No. 402879
 Seq. ID LIB3431-058-P1-K1-C12
 Method BLASTN
 NCBI GI g606816
 BLAST score 229
 E value 1.0e-126
 Match length 229
 % identity 100
 NCBI Description Oryza sativa chloroplast carbonic anhydrase mRNA, complete cds

Seq. No. 402880
 Seq. ID LIB3431-058-P1-K1-C2
 Method BLASTX
 NCBI GI g1698548
 BLAST score 664
 E value 8.0e-70
 Match length 155
 % identity 78
 NCBI Description (U58971) calmodulin-binding protein [Nicotiana tabacum]

Seq. No. 402881
 Seq. ID LIB3431-058-P1-K1-C3
 Method BLASTN
 NCBI GI g2570512
 BLAST score 283
 E value 1.0e-158

Seq. No. 402887
 Seq. ID LIB3431-058-P1-K1-C9
 Method BLASTX
 NCBI GI g5816996
 BLAST score 325
 E value 4.0e-30
 Match length 88
 % identity 73
 NCBI Description (AL110123) ribosomal protein L32-like protein [Arabidopsis thaliana]

Seq. No. 402888
 Seq. ID LIB3431-058-P1-K1-D1
 Method BLASTX
 NCBI GI g4587563
 BLAST score 301
 E value 2.0e-27
 Match length 81
 % identity 77
 NCBI Description (AC006550) Similar to gb_U51990 pre-mRNA-splicing factor hPrp18 from Homo sapiens. ESTs gb_T46391 and gb_AA721815 come from this gene. [Arabidopsis thaliana]

Seq. No. 402889
 Seq. ID LIB3431-058-P1-K1-D10
 Method BLASTN
 NCBI GI g6015437
 BLAST score 38
 E value 7.0e-12
 Match length 50
 % identity 67
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 402890
 Seq. ID LIB3431-058-P1-K1-D11
 Method BLASTX
 NCBI GI g115796
 BLAST score 482
 E value 4.0e-55
 Match length 112
 % identity 96
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi_218174_dbj_BAA00537_ (D00642) type II light-harvesting chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 402891
 Seq. ID LIB3431-058-P1-K1-D12
 Method BLASTX
 NCBI GI g6016151
 BLAST score 492
 E value 9.0e-50
 Match length 128
 % identity 77
 NCBI Description IMMUNOGLOBULIN BINDING PROTEIN HOMOLOG 3 PRECURSOR (HEAT SHOCK PROTEIN 70 HOMOLOG 3) >gi_1575130 (U58209) luminal

0984016-101000

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Seq. No.          402893
Seq. ID           LIB3431-058-P1-K1-D3
Method            BLASTN
NCBI GI           g4097337
BLAST score       304
E value           1.0e-170
Match length      368
% identity        99
NCBI Description   Oryza sativa metallothionein-like protein mRNA, complete
                  cds
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Seq. No.          402895
Seq. ID          LIB3431-058-P1-K1-D6
Method           BLASTX
NCBI GI          g1835731
BLAST score       564
E value          3.0e-58
Match length     110
% identity        99
NCBI Description  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
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Seq. No.      402896
Seq. ID      LIB3431-058-P1-K1-D7
Method       BLASTX
NCBI GI      g2130043
BLAST score   600
E value      3.0e-62
Match length  145
% identity    82
NCBI Description  Mg-chelatase chain Xantha-h - barley (fragment) >gi 847873.2
```

(U26545) Mg-chelatase subunit [Hordeum vulgare]

Seq. No. 402897
Seq. ID LIB3431-058-P1-K1-D8
Method BLASTX
NCBI GI g115787
BLAST score 679
E value 1.0e-71
Match length 152
% identity 89
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 402898
Seq. ID LIB3431-058-P1-K1-E10
Method BLASTX
NCBI GI g482311
BLAST score 551
E value 8.0e-57
Match length 109
% identity 96
NCBI Description photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No. 402899
Seq. ID LIB3431-058-P1-K1-E12
Method BLASTN
NCBI GI g20243
BLAST score 145
E value 1.0e-75
Match length 169
% identity 95
NCBI Description O.sativa GP28 gene (partial)

Seq. No. 402900
Seq. ID LIB3431-058-P1-K1-E2
Method BLASTX
NCBI GI g543711
BLAST score 191
E value 2.0e-18
Match length 86
% identity 70
NCBI Description 14-3-3-LIKE PROTEIN S94 >gi_419796_pir_S30927 14-3-3 protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140) brain specific protein [Oryza sativa]

Seq. No. 402901
Seq. ID LIB3431-058-P1-K1-E4
Method BLASTX
NCBI GI g132105
BLAST score 479
E value 3.0e-48
Match length 109

% identity 85
 NCBI Description RIBULOSE BISPHTOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 402902
 Seq. ID LIB3431-058-P1-K1-E5
 Method BLASTX
 NCBI GI g132105
 BLAST score 372
 E value 8.0e-36
 Match length 90
 % identity 82

NCBI Description RIBULOSE BISPHTOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 402903
 Seq. ID LIB3431-058-P1-K1-E7
 Method BLASTX
 NCBI GI g2570511
 BLAST score 244
 E value 7.0e-21
 Match length 86
 % identity 57

NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No. 402904
 Seq. ID LIB3431-058-P1-K1-E8
 Method BLASTX
 NCBI GI g132105
 BLAST score 396
 E value 2.0e-59
 Match length 133
 % identity 86

NCBI Description RIBULOSE BISPHTOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

```
Seq. No.      402905
Seq. ID       LIB3431-058-P1-K1-E9
Method        BLASTX
NCBI GI       g2245020
BLAST score    212
E value       7.0e-17
Match length   137
% identity     40
NCBI Description (Z97341) growth regulator like protein [Arabidopsis thaliana]
```

```
Seq. No.          402906
Seq. ID           LIB3431-058-P1-K1-F12
Method            BLASTX
NCBI GI           g3885894
BLAST score       447
E value           2.0e-44
Match length      101
% identity        87
NCBI Description   (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
```

```
Seq. No.          402907
Seq. ID          LIB3431-058-P1-K1-F2
Method          BLASTX
NCBI GI         g2501189
BLAST score      313
E value         3.0e-43
Match length     107
% identity       88
NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
                 >gi_2130146_pir_S61419 thiamine biosynthetic enzyme thil-1
                 - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                 [Zea mays]
```

```
Seq. No.      402908
Seq. ID      LIB3431-058-P1-K1-F4
Method       BLASTX
NCBI GI      g2924520
BLAST score   486
E value      6.0e-49
Match length  151
% identity    63
NCBI Description (AL022023) plasma membrane intrinsic protein (SIMIP)
               [Arabidopsis thaliana]
```

Seq. No.	402909
Seq. ID	LIB3431-058-P1-K1-F8
Method	BLASTX
NCBI GI	g3126854
BLAST score	713
E value	1.0e-75
Match length	133
% identity	98
NCBI Description	(AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	402910
Seq. ID	LIB3431-058-P1-K1-F9

Method BLASTN
 NCBI GI g3821780
 BLAST score 34
 E value 2.0e-09
 Match length 34
 % identity 100
 NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 402911
 Seq. ID LIB3431-058-P1-K1-G1
 Method BLASTN
 NCBI GI g20262
 BLAST score 300
 E value 1.0e-168
 Match length 328
 % identity 98
 NCBI Description O.sativa light-induced mRNA

Seq. No. 402912
 Seq. ID LIB3431-058-P1-K1-G10
 Method BLASTX
 NCBI GI g4581207
 BLAST score 570
 E value 6.0e-61
 Match length 145
 % identity 81
 NCBI Description (Y17914) cyclic nucleotide and calmodulin-regulated ion channel [Arabidopsis thaliana]

Seq. No. 402913
 Seq. ID LIB3431-058-P1-K1-G12
 Method BLASTX
 NCBI GI g417260
 BLAST score 416
 E value 1.0e-40
 Match length 127
 % identity 66
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

Seq. No. 402914
 Seq. ID LIB3431-058-P1-K1-G3
 Method BLASTX
 NCBI GI g4538934
 BLAST score 275
 E value 4.0e-24
 Match length 102
 % identity 53
 NCBI Description (AL049483) putative leucine-rich-repeat protein
 [Arabidopsis thaliana]

Seq. No. 402915
 Seq. ID LIB3431-058-P1-K1-G4
 Method BLASTN
 NCBI GI g3885891
 BLAST score 118


```
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]
```

Seq. No.	402920
Seq. ID	LIB3431-058-P1-K1-H12
Method	BLASTX
NCBI GI	g5916444
BLAST score	240
E value	4.0e-20
Match length	120
% identity	40
NCBI Description	(AC007633) putative protein [Arabidopsis thaliana]

```
Seq. No.      402921
Seq. ID      LIB3431-058-P1-K1-H2
Method       BLASTX
NCBI GI      g3789954
BLAST score   607
E value      3.0e-63
Match length  120
% identity    95
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]
```

Seq. No.	402922
Seq. ID	LIB3431-058-P1-K1-H6
Method	BLASTX
NCBI GI	g4585882
BLAST score	446
E value	2.0e-44
Match length	117
% identity	74
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

```
Seq. No.          402923
Seq. ID          LIB3431-058-P1-K1-H8
Method           BLASTX
NCBI GI          g132105
BLAST score      455
E value          2.0e-45
Match length     106
% identity       84
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
```

Seq. No. 402924
Seq. ID LIB3431-058-P1-K1-H9

Method BLASTX
 NCBI GI g3913018
 BLAST score 585
 E value 1.0e-60
 Match length 118
 % identity 100
 NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
 (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic
 aldolase [Oryza sativa]

Seq. No. 402925
 Seq. ID LIB3431-058-P1-N1-A1
 Method BLASTX
 NCBI GI g3355468
 BLAST score 324
 E value 2.0e-38
 Match length 106
 % identity 85
 NCBI Description (AC004218) putative ribosomal protein L35 [Arabidopsis
 thaliana]

Seq. No. 402926
 Seq. ID LIB3431-058-P1-N1-A10
 Method BLASTX
 NCBI GI g2274988
 BLAST score 281
 E value 8.0e-25
 Match length 96
 % identity 55
 NCBI Description (AJ000226) partial sequence, homology to serine
 hydroxymethyltransferases [Hordeum vulgare]

Seq. No. 402927
 Seq. ID LIB3431-058-P1-N1-A11
 Method BLASTX
 NCBI GI g517500
 BLAST score 311
 E value 1.0e-28
 Match length 77
 % identity 81
 NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa
 protein [Zea mays] >gi_444338_prf_1906386A photosystem II
 OE17 protein [Pisum sativum]

Seq. No. 402928
 Seq. ID LIB3431-058-P1-N1-A12
 Method BLASTX
 NCBI GI g3345477
 BLAST score 216
 E value 2.0e-17
 Match length 40
 % identity 100
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 402929
 Seq. ID LIB3431-058-P1-N1-A2
 Method BLASTX

NCBI GI g1514643
 BLAST score 168
 E value 3.0e-26
 Match length 144
 % identity 45
 NCBI Description (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]

Seq. No. 402930
 Seq. ID LIB3431-058-P1-N1-A3
 Method BLASTN
 NCBI GI g1159878
 BLAST score 50
 E value 7.0e-19
 Match length 82
 % identity 90
 NCBI Description A.fatua mRNA for DNA-binding protein (clone ABF2)

Seq. No. 402931
 Seq. ID LIB3431-058-P1-N1-A4
 Method BLASTN
 NCBI GI g2072554
 BLAST score 313
 E value 1.0e-175
 Match length 313
 % identity 100
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 402932
 Seq. ID LIB3431-058-P1-N1-A5
 Method BLASTN
 NCBI GI g2570510
 BLAST score 131
 E value 2.0e-67
 Match length 267
 % identity 88
 NCBI Description Oryza sativa chlorophyll a-b binding protein mRNA, complete cds

Seq. No. 402933
 Seq. ID LIB3431-058-P1-N1-A7
 Method BLASTX
 NCBI GI g671740
 BLAST score 431
 E value 2.0e-42
 Match length 80
 % identity 96
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 402934
 Seq. ID LIB3431-058-P1-N1-B10
 Method BLASTX
 NCBI GI g3885886
 BLAST score 244
 E value 1.0e-22
 Match length 53

% identity 86
NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]

Seq. No. 402935
Seq. ID LIB3431-058-P1-N1-B11
Method BLASTX
NCBI GI g2582381
BLAST score 144
E value 1.0e-08
Match length 31
% identity 87
NCBI Description (AF021220) cation-chloride co-transporter [Nicotiana tabacum]

Seq. No. 402936
Seq. ID LIB3431-058-P1-N1-B12
Method BLASTX
NCBI GI g115793
BLAST score 396
E value 2.0e-38
Match length 78
% identity 95
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR (CAB) >gi_72749_pir_CDBH3 chlorophyll a/b-binding protein type III precursor - barley >gi_19023_emb_CAA44881_ (X63197) type III LHCII CAB precursor protein [Hordeum vulgare]

Seq. No. 402937
Seq. ID LIB3431-058-P1-N1-B2
Method BLASTX
NCBI GI g3924605
BLAST score 227
E value 8.0e-19
Match length 53
% identity 72
NCBI Description (AF069442) putative inhibitor of apoptosis [Arabidopsis thaliana]

Seq. No. 402938
Seq. ID LIB3431-058-P1-N1-B5
Method BLASTX
NCBI GI g115813
BLAST score 201
E value 2.0e-15
Match length 46
% identity 83
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 402939
Seq. ID LIB3431-058-P1-N1-B6
Method BLASTX
NCBI GI g4038663
BLAST score 282
E value 4.0e-38

Match length 95
 % identity 77
 NCBI Description (AB020929) ribulose-1,5-bisphosphate carboxylase/oxygenase
 small subunit [Aegilops speltoides]

Seq. No. 402940
 Seq. ID LIB3431-058-P1-N1-B7
 Method BLASTN
 NCBI GI g21838
 BLAST score 67
 E value 3.0e-29
 Match length 207
 % identity 84
 NCBI Description T.aestivum PRK gene for ribulose-5-phosphate kinase

Seq. No. 402941
 Seq. ID LIB3431-058-P1-N1-B8
 Method BLASTX
 NCBI GI g115813
 BLAST score 265
 E value 6.0e-23
 Match length 97
 % identity 61
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
 CAB-8) >gi_19182_emb_CAA33330_(X15258) Type III
 chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 402942
 Seq. ID LIB3431-058-P1-N1-B9
 Method BLASTX
 NCBI GI g132105
 BLAST score 396
 E value 2.0e-38
 Match length 73
 % identity 99
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 402943
 Seq. ID LIB3431-058-P1-N1-C1
 Method BLASTX
 NCBI GI g2191138
 BLAST score 390
 E value 1.0e-37
 Match length 91
 % identity 78
 NCBI Description (AF007269) A_IG002N01.18 gene product [Arabidopsis
 thaliana]

Seq. No. 402944

Seq. ID LIB3431-058-P1-N1-C9
 Method BLASTX
 NCBI GI g5816996
 BLAST score 514
 E value 4.0e-52
 Match length 116
 % identity 85
 NCBI Description (AL110123) ribosomal protein L32-like protein [Arabidopsis thaliana]

Seq. No. 402950
 Seq. ID LIB3431-058-P1-N1-D10
 Method BLASTX
 NCBI GI g1617197
 BLAST score 264
 E value 7.0e-23
 Match length 71
 % identity 68
 NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 402951
 Seq. ID LIB3431-058-P1-N1-D11
 Method BLASTX
 NCBI GI g3126854
 BLAST score 249
 E value 9.0e-38
 Match length 85
 % identity 96
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 402952
 Seq. ID LIB3431-058-P1-N1-D12
 Method BLASTN
 NCBI GI g2267005
 BLAST score 269
 E value 1.0e-149
 Match length 341
 % identity 98
 NCBI Description Oryza sativa endosperm lumenal binding protein (BiP) mRNA, complete cds

Seq. No. 402953
 Seq. ID LIB3431-058-P1-N1-D2
 Method BLASTX
 NCBI GI g166341
 BLAST score 266
 E value 5.0e-23
 Match length 88
 % identity 56
 NCBI Description (M98267) alliinase [Allium cepa] >gi_1044969 (L48614) allinase [Allium cepa]

Seq. No. 402954
 Seq. ID LIB3431-058-P1-N1-D3
 Method BLASTN
 NCBI GI g4097337
 BLAST score 487

E value 0.0e+00
 Match length 495
 % identity 100
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 402955
 Seq. ID LIB3431-058-P1-N1-D4
 Method BLASTN
 NCBI GI g438246
 BLAST score 57
 E value 5.0e-23
 Match length 77
 % identity 94
 NCBI Description S.tuberosum mRNA for glycine hydroxymethyltransferase

Seq. No. 402956
 Seq. ID LIB3431-058-P1-N1-D6
 Method BLASTX
 NCBI GI g131400
 BLAST score 276
 E value 2.0e-35
 Match length 113
 % identity 62
 NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
 >gi_81471_pir_S00409 photosystem II 10K protein precursor
 - spinach >gi_170127 (J03887) 10kd polypeptide precursor
 [Spinacia oleracea]

Seq. No. 402957
 Seq. ID LIB3431-058-P1-N1-D7
 Method BLASTX
 NCBI GI g3334149
 BLAST score 206
 E value 4.0e-22
 Match length 64
 % identity 91
 NCBI Description MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR
 (MG-PROTOPORPHYRIN IX CHELATASE) >gi_2323329 (AF014053) Mg
 protoporphyrin chelatase subunit [Nicotiana tabacum]

Seq. No. 402958
 Seq. ID LIB3431-058-P1-N1-D8
 Method BLASTX
 NCBI GI g693920
 BLAST score 416
 E value 1.0e-40
 Match length 80
 % identity 97
 NCBI Description (U21113) chlorophyll a/b binding protein [Solanum tuberosum]

Seq. No. 402959
 Seq. ID LIB3431-058-P1-N1-E1
 Method BLASTX
 NCBI GI g400989
 BLAST score 544

E value 1.0e-55
 Match length 137
 % identity 73
 NCBI Description 50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR (CL24)
 >gi_322771_pir_A45113 ribosomal protein L24 precursor -
 common tobacco >gi_170273 (M87838) ribosomal protein L24
 [Nicotiana tabacum] >gi_170324 (M87839) ribosomal protein
 L24 [Nicotiana tabacum]

Seq. No. 402960
 Seq. ID LIB3431-058-P1-N1-E10
 Method BLASTX
 NCBI GI g482311
 BLAST score 502
 E value 1.0e-50
 Match length 99
 % identity 99
 NCBI Description photosystem II oxygen-evolving complex protein 1 - rice
 (strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving
 complex protein 1 [Oryza sativa]

Seq. No. 402961
 Seq. ID LIB3431-058-P1-N1-E12
 Method BLASTN
 NCBI GI g20243
 BLAST score 145
 E value 1.0e-75
 Match length 169
 % identity 95
 NCBI Description O.sativa GP28 gene (partial)

Seq. No. 402962
 Seq. ID LIB3431-058-P1-N1-E2
 Method BLASTN
 NCBI GI g303858
 BLAST score 68
 E value 9.0e-30
 Match length 147
 % identity 87
 NCBI Description Rice mRNA for brain specific protein (S94 gene), complete
 cds

Seq. No. 402963
 Seq. ID LIB3431-058-P1-N1-E4
 Method BLASTX
 NCBI GI g132105
 BLAST score 289
 E value 4.0e-49
 Match length 97
 % identity 99
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

sativa] >gi_226375_prf_1508256A ribulose biphosphate
carboxylase S [Oryza sativa]

Seq. No. 402964
Seq. ID LIB3431-058-P1-N1-E5
Method BLASTX
NCBI GI g132105
BLAST score 325
E value 2.0e-47
Match length 94
% identity 99
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf_1508256A ribulose biphosphate
carboxylase S [Oryza sativa]

Seq. No. 402965
Seq. ID LIB3431-058-P1-N1-E7
Method BLASTX
NCBI GI g115794
BLAST score 439
E value 1.0e-66
Match length 134
% identity 92
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
III CAB-13) >gi_72748_pir_CDT033 chlorophyll a/b-binding
protein type III precursor (cab-13) - tomato
>gi_19277_emb_CAA42818_ (X60275) LHCII type III
[Lycopersicon esculentum]

Seq. No. 402966
Seq. ID LIB3431-058-P1-N1-F11
Method BLASTX
NCBI GI g2245106
BLAST score 328
E value 2.0e-30
Match length 80
% identity 70
NCBI Description (Z97343) thioesterase like protein [Arabidopsis thaliana]

Seq. No. 402967
Seq. ID LIB3431-058-P1-N1-F12
Method BLASTX
NCBI GI g3885894
BLAST score 517
E value 2.0e-52
Match length 115
% identity 87
NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No. 402968
Seq. ID LIB3431-058-P1-N1-F2

Method BLASTX
 NCBI GI g2501190
 BLAST score 325
 E value 6.0e-30
 Match length 85
 % identity 81
 NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
 >gi_2130147_pir_S61420 thiamine biosynthetic enzyme thil-2
 - maize >gi_596080 (U17351) thiamine biosynthetic enzyme
 [Zea mays]

Seq. No. 402969
 Seq. ID LIB3431-058-P1-N1-F3
 Method BLASTX
 NCBI GI g115871
 BLAST score 236
 E value 2.0e-31
 Match length 103
 % identity 60
 NCBI Description [Segment 2 of 2] SERINE CARBOXYPEPTIDASE II CHAINS A AND B
 (CARBOXYPEPTIDASE D) (CPDW-II) (CP-WII)
 >gi_82623_pir_B29639 serine-type carboxypeptidase (EC
 3.4.16.1) II B chain - wheat >gi_1421108_pdb_1BCR_B Chain
 B, Complex Of The Wheat Serine Carboxypeptidase, Cpdw-Ii,
 With The Microbial Peptide Aldehyde Inhibitor, Antipain,
 And Arginine At Room Temperature >gi_1421113_pdb_1BCS_B
 Chain B, Complex Of The Wheat Serine Carboxypeptidase,
 Cpdw-Ii, With The Microbial Peptide Aldehyde Inhibitor,
 Chymostatin, And Arginine At 100 Degrees Kelvin
 >gi_226041_prf_1408164B CPase II B [Triticum aestivum]

Seq. No. 402970
 Seq. ID LIB3431-058-P1-N1-F4
 Method BLASTX
 NCBI GI g3158476
 BLAST score 217
 E value 8.0e-31
 Match length 89
 % identity 78
 NCBI Description (AF067185) aquaporin 2 [Samanea saman]

Seq. No. 402971
 Seq. ID LIB3431-058-P1-N1-F5
 Method BLASTX
 NCBI GI g4960154
 BLAST score 318
 E value 4.0e-29
 Match length 73
 % identity 85
 NCBI Description (AF153283) putative progesterone-binding protein homolog
 [Arabidopsis thaliana]

Seq. No. 402972
 Seq. ID LIB3431-058-P1-N1-F6
 Method BLASTN
 NCBI GI g505134
 BLAST score 209

E value 1.0e-114
 Match length 305
 % identity 93
 NCBI Description Rice mRNA for ferredoxin, complete cds

Seq. No. 402973
 Seq. ID LIB3431-058-P1-N1-F8
 Method BLASTX
 NCBI GI g3126854
 BLAST score 411
 E value 4.0e-54
 Match length 113
 % identity 96
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 402974
 Seq. ID LIB3431-058-P1-N1-G1
 Method BLASTX
 NCBI GI g417260
 BLAST score 255
 E value 1.0e-24
 Match length 79
 % identity 69
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

Seq. No. 402975
 Seq. ID LIB3431-058-P1-N1-G10
 Method BLASTX
 NCBI GI g517500
 BLAST score 301
 E value 2.0e-27
 Match length 89
 % identity 70
 NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa
 protein [Zea mays] >gi_444338_prf_1906386A photosystem II
 OE17 protein [Pisum sativum]

Seq. No. 402976
 Seq. ID LIB3431-058-P1-N1-G12
 Method BLASTX
 NCBI GI g417260
 BLAST score 411
 E value 5.0e-40
 Match length 128
 % identity 66
 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir_S33632
 lirl protein - rice >gi_20263_emb_CAA48706_ (X68807)
 light-regulated gene [Oryza sativa]

Seq. No. 402977
 Seq. ID LIB3431-058-P1-N1-G4
 Method BLASTX
 NCBI GI g3885892
 BLAST score 513
 E value 4.0e-52

Match length 96
 % identity 100
 NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 402978
 Seq. ID LIB3431-058-P1-N1-G8
 Method BLASTX
 NCBI GI g548603
 BLAST score 543
 E value 1.0e-55
 Match length 108
 % identity 95
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
 (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
 >gi_478404_pir_JQ2247 photosystem I chain D precursor -
 barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 402979
 Seq. ID LIB3431-058-P1-N1-G9
 Method BLASTX
 NCBI GI g3004565
 BLAST score 188
 E value 2.0e-18
 Match length 94
 % identity 52
 NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 402980
 Seq. ID LIB3431-058-P1-N1-H11
 Method BLASTX
 NCBI GI g132105
 BLAST score 234
 E value 4.0e-21
 Match length 70
 % identity 81
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 402981
 Seq. ID LIB3431-058-P1-N1-H2
 Method BLASTX
 NCBI GI g3789954
 BLAST score 339
 E value 1.0e-54
 Match length 110
 % identity 95
 NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza
 sativa]

Seq. No. 402982

Seq. ID LIB3431-058-P1-N1-H8
 Method BLASTX
 NCBI GI g132105
 BLAST score 482
 E value 2.0e-48
 Match length 99
 % identity 89
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 402983
 Seq. ID LIB3431-058-P1-N1-H9
 Method BLASTX
 NCBI GI g2407279
 BLAST score 206
 E value 4.0e-16
 Match length 43
 % identity 98
 NCBI Description (AF017362) aldolase [Oryza sativa]

Seq. No. 402984
 Seq. ID LIB3431-059-P1-K1-A10
 Method BLASTX
 NCBI GI g115787
 BLAST score 571
 E value 4.0e-59
 Match length 111
 % identity 98
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 402985
 Seq. ID LIB3431-059-P1-K1-A11
 Method BLASTX
 NCBI GI g6006871
 BLAST score 333
 E value 4.0e-31
 Match length 126
 % identity 52
 NCBI Description (AC009540) hypothetical protein [Arabidopsis thaliana] >gi_6091753_gb_AAF03463.1_AC009327_2 (AC009327) hypothetical protein [Arabidopsis thaliana]

Seq. No. 402986
 Seq. ID LIB3431-059-P1-K1-A12
 Method BLASTX
 NCBI GI g3789952

E value	8.0e-53
Match length	121
% identity	82
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

```
Seq. No.      403031
Seq. ID       LIB3431-059-P1-K1-F1
Method        BLASTX
NCBI GI       g1173347
BLAST score   593
E value       2.0e-61
Match length  130
% identity    91
NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC
                3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                aestivum]
```

```
Seq. No.      403032
Seq. ID      LIB3431-059-P1-K1-F10
Method       BLASTX
NCBI GI      g3288821
BLAST score   484
E value      9.0e-49
Match length  132
% identity    72
NCBI Description (AF063901) alanine:glyoxylate aminotransferase;
transaminase [Arabidopsis thaliana]
>gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209)
alanine-glyoxylate aminotransferase [Arabidopsis thaliana]
```

```
Seq. No.          403033
Seq. ID           LIB3431-059-P1-K1-F11
Method            BLASTN
NCBI GI           g6015437
BLAST score       35
E value           4.0e-10
Match length      35
% identity        100
NCBI Description   Homo sapiens PEX1 mRNA, complete cds
```

```
Seq. No.      403034
Seq. ID      LIB3431-059-P1-K1-F12
Method       BLASTN
NCBI GI      g1245938
BLAST score   35
E value      4.0e-10
Match length  35
% identity    100
NCBI Description  rabClC-2 beta=chloride channel ClC-2G isoform [rabbits,
heart atrium, mRNA, 2998 nt]
```

Seq. No. 403035
Seq. ID LIB3431-059-P1-K1-F3

Method BLASTX
 NCBI GI g1800227
 BLAST score 246
 E value 6.0e-21
 Match length 67
 % identity 60
 NCBI Description (U76004) Bowman-Birk proteinase inhibitor [Oryza sativa]

Seq. No. 403036
 Seq. ID LIB3431-059-P1-K1-F4
 Method BLASTX
 NCBI GI g115787
 BLAST score 519
 E value 7.0e-53
 Match length 120
 % identity 87
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 403037
 Seq. ID LIB3431-059-P1-K1-F5
 Method BLASTX
 NCBI GI g132105
 BLAST score 395
 E value 2.0e-38
 Match length 73
 % identity 99
 NCBI Description RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 403038
 Seq. ID LIB3431-059-P1-K1-F6
 Method BLASTN
 NCBI GI g3819345
 BLAST score 60
 E value 7.0e-25
 Match length 168
 % identity 84
 NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG0803

Seq. No. 403039
 Seq. ID LIB3431-059-P1-K1-G2
 Method BLASTX
 NCBI GI g132105
 BLAST score 429
 E value 2.0e-42
 Match length 104

000101-910100

Match length 67
 % identity 82
 NCBI Description (X66012) cathepsin B [Triticum aestivum]

Seq. No. 403045
 Seq. ID LIB3431-059-P1-K1-H12
 Method BLASTX
 NCBI GI g4567283
 BLAST score 270
 E value 8.0e-24
 Match length 125
 % identity 46
 NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]

Seq. No. 403046
 Seq. ID LIB3431-059-P1-K1-H2
 Method BLASTX
 NCBI GI g2582822
 BLAST score 213
 E value 6.0e-17
 Match length 53
 % identity 74
 NCBI Description (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]

Seq. No. 403047
 Seq. ID LIB3431-059-P1-K1-H4
 Method BLASTX
 NCBI GI g115772
 BLAST score 298
 E value 1.0e-34
 Match length 96
 % identity 83
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi_82460_pir_S03705 chlorophyll a/b-binding protein 1R precursor - rice >gi_20178_emb_CAA32108 (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235) [Oryza sativa]

Seq. No. 403048
 Seq. ID LIB3431-059-P1-K1-H5
 Method BLASTX
 NCBI GI g871931
 BLAST score 281
 E value 4.0e-25
 Match length 77
 % identity 78
 NCBI Description (D30763) ferredoxin [Oryza sativa]

Seq. No. 403049
 Seq. ID LIB3431-059-P1-K1-H7
 Method BLASTX
 NCBI GI g131773
 BLAST score 583
 E value 2.0e-60
 Match length 122
 % identity 97

09684015.101000

NCBI Description 40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
>gi_82724_pir__B30097 ribosomal protein S14 (clone MCH2) -
maize

Seq. No. 403050
Seq. ID LIB3431-059-P1-K1-H8
Method BLASTN
NCBI GI g6015437
BLAST score 38
E value 9.0e-12
Match length 49
% identity 66
NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 403051
Seq. ID LIB3431-059-P1-K1-H9
Method BLASTX
NCBI GI g3894197
BLAST score 346
E value 1.0e-32
Match length 139
% identity 49
NCBI Description (AC005662) hypothetical protein [Arabidopsis thaliana]

Seq. No. 403052
Seq. ID LIB3431-059-P1-N1-A1
Method BLASTX
NCBI GI g115813
BLAST score 257
E value 3.0e-22
Match length 61
% identity 82
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 403053
Seq. ID LIB3431-059-P1-N1-A10
Method BLASTX
NCBI GI g421916
BLAST score 190
E value 2.0e-14
Match length 36
% identity 97
NCBI Description chlorophyll a/b-binding protein - English ivy (fragment)
>gi_12582_emb_CAA48410_ (X68333) light harvesting
chlorophyll a/b binding protein [Hedera helix]

Seq. No. 403054
Seq. ID LIB3431-059-P1-N1-A12
Method BLASTN
NCBI GI g3789951
BLAST score 160
E value 1.0e-84
Match length 362
% identity 99
NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor

E value 1.0e-123
 Match length 248
 % identity 98
 NCBI Description Oryza sativa mRNA for glycine-rich RNA-binding protein (OsGRP1)

Seq. No. 403066
 Seq. ID LIB3431-059-P1-N1-B7
 Method BLASTX
 NCBI GI g3885894
 BLAST score 193
 E value 1.0e-14
 Match length 53
 % identity 75
 NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No. 403067
 Seq. ID LIB3431-059-P1-N1-B8
 Method BLASTX
 NCBI GI g1351270
 BLAST score 195
 E value 6.0e-15
 Match length 48
 % identity 85
 NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
 >gi_478410_pir_JQ2255 triose-phosphate isomerase (EC 5.3.1.1) - rice >gi_169821 (M87064) triosephosphate isomerase [Oryza sativa]

Seq. No. 403068
 Seq. ID LIB3431-059-P1-N1-C1
 Method BLASTN
 NCBI GI g3617841
 BLAST score 186
 E value 1.0e-100
 Match length 190
 % identity 99
 NCBI Description Oryza sativa clone F14605 calmodulin (CaM1) mRNA, complete cds

Seq. No. 403069
 Seq. ID LIB3431-059-P1-N1-C10
 Method BLASTX
 NCBI GI g347451
 BLAST score 197
 E value 3.0e-15
 Match length 37
 % identity 100
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 403070
 Seq. ID LIB3431-059-P1-N1-C12
 Method BLASTX
 NCBI GI g3885892
 BLAST score 266
 E value 3.0e-23

Match length 53
% identity 100
NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

```
Seq. No.      403071
Seq. ID      LIB3431-059-P1-N1-C2
Method       BLASTN
NCBI GI      g4079797
BLAST score   39
E value      2.0e-12
Match length  71
% identity    89
NCBI Description  Oryza sativa 23 kDa polypeptide of photosystem II mRNA,
complete cds
```

```
Seq. No.          403072
Seq. ID          LIB3431-059-P1-N1-C6
Method          BLASTX
NCBI GI         g2570511
BLAST score      163
E value         3.0e-22
Match length     67
% identity       78
NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]
```

Seq. No.	403073
Seq. ID	LIB3431-059-P1-N1-C7
Method	BLASTN
NCBI GI	g20262
BLAST score	126
E value	2.0e-64
Match length	194
% identity	91
NCBI Description	O.sativa light-induced mRNA

Seq. No.	403074
Seq. ID	LIB3431-059-P1-N1-C8
Method	BLASTX
NCBI GI	g3885894
BLAST score	193
E value	1.0e-14
Match length	53
% identity	75
NCBI Description	(AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

```
Seq. No.      403075
Seq. ID      LIB3431-059-P1-N1-C9
Method       BLASTX
NCBI GI      g3138799
BLAST score   263
E value      7.0e-23
Match length  60
% identity    87
NCBI Description (AB014058) beta 6 subunit of 20S proteasome [Oryza sativa]
```

Seq. No.	403076
Seq. ID	LIB3431-059-P1-N1-D10

Method BLASTN
 NCBI GI g2072554
 BLAST score 380
 E value 0.0e+00
 Match length 380
 % identity 100
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 403077
 Seq. ID LIB3431-059-P1-N1-D11
 Method BLASTX
 NCBI GI g671740
 BLAST score 243
 E value 1.0e-20
 Match length 47
 % identity 100
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 403078
 Seq. ID LIB3431-059-P1-N1-D12
 Method BLASTX
 NCBI GI g3915826
 BLAST score 202
 E value 9.0e-16
 Match length 41
 % identity 100
 NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 403079
 Seq. ID LIB3431-059-P1-N1-D3
 Method BLASTX
 NCBI GI g548605
 BLAST score 386
 E value 2.0e-37
 Match length 80
 % identity 95
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir_A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No. 403080
 Seq. ID LIB3431-059-P1-N1-D4
 Method BLASTX
 NCBI GI g132105
 BLAST score 526
 E value 1.0e-53
 Match length 95
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate

Match length 102
 % identity 86
 NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S7
 >gi_2119068_pir_S58630 ribosomal protein S7 - maize
 chloroplast >gi_902274_emb_CAA60339_ (X86563) ribosomal
 protein S7 [Zea mays] >gi_902298_emb_CAA60362_ (X86563)
 ribosomal protein S7 [Zea mays]

Seq. No. 403091
 Seq. ID LIB3431-059-P1-N1-E7
 Method BLASTX
 NCBI GI g1835731
 BLAST score 286
 E value 1.0e-25
 Match length 65
 % identity 85
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 403092
 Seq. ID LIB3431-059-P1-N1-E9
 Method BLASTX
 NCBI GI g733454
 BLAST score 232
 E value 3.0e-19
 Match length 48
 % identity 94
 NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
 [Zea mays]

Seq. No. 403093
 Seq. ID LIB3431-059-P1-N1-F1
 Method BLASTX
 NCBI GI g1173347
 BLAST score 216
 E value 2.0e-17
 Match length 47
 % identity 94
 NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
 (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
 >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC
 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
 (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
 aestivum]

Seq. No. 403094
 Seq. ID LIB3431-059-P1-N1-F10
 Method BLASTX
 NCBI GI g2754849
 BLAST score 199
 E value 2.0e-15
 Match length 45
 % identity 87
 NCBI Description (AF039000) putative serine-glyoxylate aminotransferase
 [Fritillaria agrestis]

Seq. No. 403095
 Seq. ID LIB3431-059-P1-N1-F4

Method BLASTX
 NCBI GI g3036951
 BLAST score 199
 E value 9.0e-19
 Match length 52
 % identity 98
 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 403096
 Seq. ID LIB3431-059-P1-N1-F5
 Method BLASTX
 NCBI GI g671740
 BLAST score 336
 E value 2.0e-31
 Match length 64
 % identity 95
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 403097
 Seq. ID LIB3431-059-P1-N1-F7
 Method BLASTN
 NCBI GI g606816
 BLAST score 306
 E value 1.0e-172
 Match length 326
 % identity 98
 NCBI Description Oryza sativa chloroplast carbonic anhydrase mRNA, complete cds

Seq. No. 403098
 Seq. ID LIB3431-059-P1-N1-F8
 Method BLASTX
 NCBI GI g517500
 BLAST score 378
 E value 2.0e-36
 Match length 91
 % identity 81
 NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf_1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No. 403099
 Seq. ID LIB3431-059-P1-N1-G11
 Method BLASTX
 NCBI GI g4079798
 BLAST score 326
 E value 3.0e-30
 Match length 65
 % identity 97
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 403100
 Seq. ID LIB3431-059-P1-N1-G2
 Method BLASTX

```

NCBI GI          g347451
BLAST score      248
E value         4.0e-21
Match length     48
% identity       100
NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                  sativa]

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```
Seq. No.          403101
Seq. ID           LIB3431-059-P1-N1-G3
Method            BLASTX
NCBI GI           g115787
BLAST score       329
E value           1.0e-30
Match length      63
% identity        100
NCBI Description   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA_28 to 235)
                  [Oryza sativa]
```

Seq. No.	403102
Seq. ID	LIB3431-059-P1-N1-G7
Method	BLASTX
NCBI GI	g3450889
BLAST score	279
E value	9.0e-25
Match length	63
% identity	86
NCBI Description	(AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

```
Seq. No.      403103
Seq. ID       LIB3431-059-P1-N1-G9
Method        BLASTX
NCBI GI       g21839
BLAST score    163
E value       3.0e-11
Match length   35
% identity     94
NCBI Description (X57952) phosphoribulokinase [Triticum aestivum]
```

Seq. No.	403104
Seq. ID	LIB3431-059-P1-N1-H1
Method	BLASTX
NCBI GI	g4455232
BLAST score	151
E value	9.0e-10
Match length	36
% identity	75
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

```
Seq. No.      403105
Seq. ID      LIB3431-059-P1-N1-H10
Method       BLASTX
NCBI GI      g3345477
BLAST score   172
```


Seq. No. 403116
Seq. ID LIB3431-060-P1-K1-A5
Method BLASTX
NCBI GI g5262202
BLAST score 220
E value 8.0e-18
Match length 127
% identity 39
NCBI Description (AL080252) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 403117
Seq. ID LIB3431-060-P1-K1-A6
Method BLASTX
NCBI GI g671740
BLAST score 280
E value 8.0e-25
Match length 49
% identity 100
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 403118
Seq. ID LIB3431-060-P1-K1-A7
Method BLASTX
NCBI GI g2673914
BLAST score 287
E value 1.0e-25
Match length 122
% identity 47
NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No. 403119
Seq. ID LIB3431-060-P1-K1-A8
Method BLASTX
NCBI GI g3201612
BLAST score 153
E value 5.0e-10
Match length 60
% identity 50
NCBI Description (AC004669) putative 2A6 protein [Arabidopsis thaliana]

Seq. No. 403120
Seq. ID LIB3431-060-P1-K1-B10
Method BLASTX
NCBI GI g2570511
BLAST score 637
E value 1.0e-66
Match length 120
% identity 99
NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No. 403121
Seq. ID LIB3431-060-P1-K1-B5
Method BLASTX
NCBI GI g115787
BLAST score 481

Seq. No.	403126
Seq. ID	LIB3431-060-P1-K1-C11
Method	BLASTX
NCBI GI	g2980641
BLAST score	174
E value	2.0e-12
Match length	76
% identity	50
NCBI Description	(Y11250) multi resistance protein [Arabidopsis thaliana]
Seq. No.	403127
Seq. ID	LIB3431-060-P1-K1-C12
Method	BLASTX
NCBI GI	g3789954
BLAST score	610
E value	1.0e-63
Match length	113
% identity	100
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]
Seq. No.	403128
Seq. ID	LIB3431-060-P1-K1-C4
Method	BLASTX
NCBI GI	g2072555
BLAST score	237
E value	7.0e-20
Match length	44
% identity	100
NCBI Description	(AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]
Seq. No.	403129
Seq. ID	LIB3431-060-P1-K1-C6
Method	BLASTX
NCBI GI	g3885886
BLAST score	632
E value	3.0e-66
Match length	123
% identity	100
NCBI Description	(AF093631) Rieske Fe-S precursor protein [Oryza sativa]
Seq. No.	403130
Seq. ID	LIB3431-060-P1-K1-C7
Method	BLASTX
NCBI GI	g4200165
BLAST score	563
E value	5.0e-58
Match length	134
% identity	79
NCBI Description	(Y16262) neutral invertase [Daucus carota]
Seq. No.	403131
Seq. ID	LIB3431-060-P1-K1-C8
Method	BLASTX

[Hordeum vulgare]

Seq. No. 403136
 Seq. ID LIB3431-060-P1-K1-D7
 Method BLASTN
 NCBI GI g20239
 BLAST score 141
 E value 3.0e-73
 Match length 169
 % identity 96
 NCBI Description O.sativa (rice) shoot-specific GOS5 gene for a putative chloroplast transit peptide

Seq. No. 403137
 Seq. ID LIB3431-060-P1-K1-D8
 Method BLASTX
 NCBI GI g4587579
 BLAST score 251
 E value 2.0e-21
 Match length 143
 % identity 35
 NCBI Description (AC006550) F1003.1 [Arabidopsis thaliana]

Seq. No. 403138
 Seq. ID LIB3431-060-P1-K1-D9
 Method BLASTN
 NCBI GI g6015437
 BLAST score 36
 E value 4.0e-11
 Match length 44
 % identity 64
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 403139
 Seq. ID LIB3431-060-P1-K1-E1
 Method BLASTX
 NCBI GI g4559358
 BLAST score 341
 E value 5.0e-32
 Match length 97
 % identity 63
 NCBI Description (AC006585) putative steroid binding protein [Arabidopsis thaliana]

Seq. No. 403140
 Seq. ID LIB3431-060-P1-K1-E10
 Method BLASTX
 NCBI GI g1488297
 BLAST score 190
 E value 3.0e-14
 Match length 132
 % identity 36
 NCBI Description (U63530) osRAD23 [Oryza sativa]

Seq. No. 403141
 Seq. ID LIB3431-060-P1-K1-E2
 Method BLASTX

0689-016

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Seq. No.          403150
Seq. ID           LIB3431-060-P1-K1-F5
Method            BLASTX
NCBI GI           g3789952
BLAST score       516
E value           1.0e-52
Match length      103
% identity        98
```


Seq. No. 403159
 Seq. ID LIB3431-060-P1-K1-G3
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 9.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 403160
 Seq. ID LIB3431-060-P1-K1-G5
 Method BLASTX
 NCBI GI g2407281
 BLAST score 700
 E value 4.0e-74
 Match length 131
 % identity 99
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
 subunit [Oryza sativa]

Seq. No. 403161
 Seq. ID LIB3431-060-P1-K1-G6
 Method BLASTX
 NCBI GI g2501189
 BLAST score 257
 E value 3.0e-22
 Match length 121
 % identity 58
 NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
 >gi_2130146_pir_S61419 thiamine biosynthetic enzyme thil-1
 - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
 [Zea mays]

Seq. No. 403162
 Seq. ID LIB3431-060-P1-K1-G7
 Method BLASTX
 NCBI GI g4544428
 BLAST score 214
 E value 3.0e-17
 Match length 51
 % identity 76
 NCBI Description (AC006955) unknown protein [Arabidopsis thaliana]

Seq. No. 403163
 Seq. ID LIB3431-060-P1-K1-G8
 Method BLASTX
 NCBI GI g1053047
 BLAST score 591
 E value 3.0e-61
 Match length 118
 % identity 100
 NCBI Description (U38425) histone H3 [Glycine max] >gi_1053049 (U38426)
 histone H3 [Glycine max] >gi_1053051 (U38427) histone H3
 [Glycine max]

000101-91048950

NCBI Description Rice complete chloroplast genome

Seq. No. 403178
 Seq. ID LIB3431-060-P1-N1-B5
 Method BLASTN
 NCBI GI g20181
 BLAST score 163
 E value 2.0e-86
 Match length 177
 % identity 98

NCBI Description Rice cab2R gene for light harvesting chlorophyll
 a/b-binding protein

Seq. No. 403179
 Seq. ID LIB3431-060-P1-N1-B7
 Method BLASTX
 NCBI GI g115787
 BLAST score 559
 E value 2.0e-57
 Match length 111
 % identity 97

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding
 protein 2R precursor - rice >gi_20182_emb_CAA32109
 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
 [Oryza sativa]

Seq. No. 403180
 Seq. ID LIB3431-060-P1-N1-C1
 Method BLASTN
 NCBI GI g3885887
 BLAST score 221
 E value 1.0e-121
 Match length 296
 % identity 93

NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
 complete cds

Seq. No. 403181
 Seq. ID LIB3431-060-P1-N1-C10
 Method BLASTX
 NCBI GI g1619300
 BLAST score 174
 E value 2.0e-12
 Match length 48
 % identity 65

NCBI Description (X95269) LRR protein [Lycopersicon esculentum]

Seq. No. 403182
 Seq. ID LIB3431-060-P1-N1-C11
 Method BLASTX
 NCBI GI g2316016
 BLAST score 150
 E value 2.0e-09
 Match length 71
 % identity 44

NCBI Description (U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. ID LIB3431-060-P1-N1-D1
 Method BLASTX
 NCBI GI g3913811
 BLAST score 367
 E value 4.0e-35
 Match length 91
 % identity 84
 NCBI Description GLUTAMYL-TRNA REDUCTASE PRECURSOR (GLUTR)
 >gi_2920320_dbj_BAA25003_ (AB011416) glutamyl-tRNA
 reductase [*Oryza sativa*]

Seq. No. 403189
 Seq. ID LIB3431-060-P1-N1-D12
 Method BLASTX
 NCBI GI g3126854
 BLAST score 345
 E value 1.0e-32
 Match length 65
 % identity 100
 NCBI Description (AF061577) chlorophyll a/b binding protein [*Oryza sativa*]

Seq. No. 403190
 Seq. ID LIB3431-060-P1-N1-D2
 Method BLASTX
 NCBI GI g266567
 BLAST score 306
 E value 8.0e-28
 Match length 87
 % identity 66
 NCBI Description MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR
 (ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II)
 >gi_421956_pir_S23558 mitochondrial processing peptidase
 (EC 3.4.99.41) alpha chain precursor - potato
 >gi_21493_emb_CAA46990_ (X66284) mitochondrial processing
 peptidase [*Solanum tuberosum*]

Seq. No. 403191
 Seq. ID LIB3431-060-P1-N1-D4
 Method BLASTX
 NCBI GI g733456
 BLAST score 352
 E value 2.0e-33
 Match length 73
 % identity 95
 NCBI Description (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
 [*Zea mays*]

Seq. No. 403192
 Seq. ID LIB3431-060-P1-N1-D8
 Method BLASTX
 NCBI GI g3850577
 BLAST score 185
 E value 6.0e-16
 Match length 120
 % identity 41
 NCBI Description (AC005278) This gene may be cut off. [*Arabidopsis thaliana*]


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NCBI GI      g5006852
BLAST score   225
E value      1.0e-123
Match length 293
% identity   94
NCBI Description Oryza sativa homeodomain leucine zipper protein (hox4)
                mRNA, complete cds

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Seq. No.      403204
Seq. ID      LIB3431-060-P1-N1-G2
Method       BLASTX
NCBI GI      g131192
BLAST score   209
E value      2.0e-16
Match length  44
% identity    86
NCBI Description  PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR
                  (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi_100606_pir__S20937
                  photosystem I chain V precursor - barley
                  >gi_19091_emb_CAA42727_ (X60158) photosystem I polypeptide
                  PSI-G precursor [Hordeum vulgare]
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Seq. No.          403205
Seq. ID           LIB3431-060-P1-N1-G3
Method            BLASTX
NCBI GI           g2072555
BLAST score       237
E value           1.0e-19
Match length      44
% identity         100
NCBI Description  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
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Seq. No.      403206
Seq. ID       LIB3431-060-P1-N1-G5
Method        BLASTX
NCBI GI       g132105
BLAST score   186
E value       6.0e-14
Match length  35
% identity    100
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]

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Seq. No.      403207
Seq. ID      LIB3431-060-P1-N1-G7
Method       BLASTX
NCBI GI      g4544428
BLAST score  294
```

E value 2.0e-26
 Match length 81
 % identity 69
 NCBI Description (AC006955) unknown protein [Arabidopsis thaliana]

Seq. No. 403208
 Seq. ID LIB3431-060-P1-N1-G8
 Method BLASTX
 NCBI GI g417103
 BLAST score 283
 E value 4.0e-25
 Match length 58
 % identity 98
 NCBI Description HISTONE H3.2, MINOR >gi_282871_pir_S24346 histone H3.3-like protein - Arabidopsis thaliana
 >gi_16324_emb_CAA42957_(X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_(X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_(X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_(X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380 (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1 (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1 (AL035708) Histon H3 [Arabidopsis thaliana] >gi_6006364_dbj_BAA84794.1 (AP000559) EST D15300(C0425) corresponds to a region of the predicted gene.; Similar to histone H3 (AB015760) [Oryza sativa]

Seq. No. 403209
 Seq. ID LIB3431-060-P1-N1-H10
 Method BLASTX
 NCBI GI g671740
 BLAST score 499
 E value 2.0e-50
 Match length 91
 % identity 99
 NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 403210
 Seq. ID LIB3431-060-P1-N1-H11
 Method BLASTX
 NCBI GI g3036951
 BLAST score 282
 E value 3.0e-25
 Match length 54
 % identity 100
 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana glauca]

Method BLASTX
 NCBI GI g132105
 BLAST score 327
 E value 8.0e-41
 Match length 108
 % identity 83
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 403217
 Seq. ID LIB3431-061-P1-K1-A11
 Method BLASTX
 NCBI GI g3345477
 BLAST score 232
 E value 2.0e-19
 Match length 85
 % identity 55
 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 403218
 Seq. ID LIB3431-061-P1-K1-A12
 Method BLASTX
 NCBI GI g82080
 BLAST score 310
 E value 1.0e-28
 Match length 90
 % identity 68
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf_1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]

Seq. No. 403219
 Seq. ID LIB3431-061-P1-K1-A2
 Method BLASTX
 NCBI GI g4455248
 BLAST score 150
 E value 1.0e-09
 Match length 69
 % identity 51
 NCBI Description (AL035523) acyl carrier-like protein [Arabidopsis thaliana]

Seq. No. 403220
 Seq. ID LIB3431-061-P1-K1-A3
 Method BLASTX
 NCBI GI g3913018
 BLAST score 570
 E value 7.0e-59
 Match length 115
 % identity 100
 NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Match length 103
% identity 81
NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
[Zea mays]

Seq. No. 403231
Seq. ID LIB3431-061-P1-K1-C10
Method BLASTX
NCBI GI g4586058
BLAST score 209
E value 2.0e-17
Match length 116
% identity 46
NCBI Description (AC007020) unknown protein [Arabidopsis thaliana]

Seq. No. 403232
Seq. ID LIB3431-061-P1-K1-C12
Method BLASTN
NCBI GI g2072554
BLAST score 47
E value 3.0e-17
Match length 199
% identity 81
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
cds

Seq. No. 403233
Seq. ID LIB3431-061-P1-K1-C2
Method BLASTX
NCBI GI g1052960
BLAST score 748
E value 1.0e-79
Match length 146
% identity 91
NCBI Description (U37437) PNIL34 [Ipomoea nil]

Seq. No. 403234
Seq. ID LIB3431-061-P1-K1-C3
Method BLASTN
NCBI GI g1304214
BLAST score 51
E value 1.0e-19
Match length 95
% identity 88
NCBI Description Rice mRNA for precursor of 22 kDa protein of photosystem II
(PSII-S), complete cds

Seq. No. 403235
Seq. ID LIB3431-061-P1-K1-C4
Method BLASTX
NCBI GI g729668
BLAST score 197
E value 3.0e-15
Match length 58
% identity 60
NCBI Description HISTONE H1 >gi_2147479_pir_S65059 histone H1,
drought-inducible - Lycopersicon pennellii >gi_436823

NCBI GI g6015437
 BLAST score 36
 E value 1.0e-10
 Match length 47
 % identity 65
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 403266
 Seq. ID LIB3431-061-P1-K1-F9
 Method BLASTN
 NCBI GI g6015437
 BLAST score 40
 E value 4.0e-13
 Match length 40
 % identity 100
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 403267
 Seq. ID LIB3431-061-P1-K1-G1
 Method BLASTN
 NCBI GI g4138289
 BLAST score 300
 E value 1.0e-168
 Match length 312
 % identity 99
 NCBI Description Oryza sativa mRNA for thioredoxin M

Seq. No. 403268
 Seq. ID LIB3431-061-P1-K1-G10
 Method BLASTX
 NCBI GI g4105561
 BLAST score 568
 E value 1.0e-58
 Match length 127
 % identity 89
 NCBI Description (AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]

Seq. No. 403269
 Seq. ID LIB3431-061-P1-K1-G11
 Method BLASTX
 NCBI GI g320618
 BLAST score 409
 E value 5.0e-40
 Match length 98
 % identity 80
 NCBI Description chlorophyll a/b-binding protein I precursor - rice
 >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
 chlorophyll a/b-binding protein [Oryza sativa]
 >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
 [Oryza sativa]

Seq. No. 403270
 Seq. ID LIB3431-061-P1-K1-G12
 Method BLASTX
 NCBI GI g3057120
 BLAST score 256
 E value 2.0e-22

sativa]

Seq. No. 403286
 Seq. ID LIB3431-062-P1-K1-A12
 Method BLASTX
 NCBI GI g5360591
 BLAST score 476
 E value 9.0e-48
 Match length 149
 % identity 60
 NCBI Description (AB022328) nClpP3 [Arabidopsis thaliana]

Seq. No. 403287
 Seq. ID LIB3431-062-P1-K1-A2
 Method BLASTX
 NCBI GI g419742
 BLAST score 624
 E value 3.0e-65
 Match length 127
 % identity 91
 NCBI Description protochlorophyllide reductase (EC 1.3.1.33) precursor -
 loblolly pine

Seq. No. 403288
 Seq. ID LIB3431-062-P1-K1-A3
 Method BLASTX
 NCBI GI g548603
 BLAST score 434
 E value 7.0e-43
 Match length 130
 % identity 70
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
 (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
 >gi_478404_pir_JQ2247 photosystem I chain D precursor -
 barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 403289
 Seq. ID LIB3431-062-P1-K1-A7
 Method BLASTX
 NCBI GI g1835731
 BLAST score 180
 E value 9.0e-14
 Match length 44
 % identity 80
 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 403290
 Seq. ID LIB3431-062-P1-K1-A8
 Method BLASTX
 NCBI GI g3126854
 BLAST score 648
 E value 1.0e-73
 Match length 150
 % identity 93
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 403291

BLAST score 204
 E value 6.0e-16
 Match length 130
 % identity 45
 NCBI Description (AB023482) ESTs AU058081(E30812), AU058365(E50679), AU030138(E50679) correspond to a region of the predicted gene.; Similar to Spinacia oleracea mRNA for proteasome 37kD subunit.(X96974) [Oryza sativa]

Seq. No. 403302
 Seq. ID LIB3431-062-P1-K1-C5
 Method BLASTX
 NCBI GI g132105
 BLAST score 553
 E value 7.0e-57
 Match length 120
 % identity 87
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 403303
 Seq. ID LIB3431-062-P1-K1-C6
 Method BLASTX
 NCBI GI g1854378
 BLAST score 252
 E value 1.0e-25
 Match length 125
 % identity 56
 NCBI Description (AB001338) Sucrose-Phosphate Synthase [Saccharum officinarum]

Seq. No. 403304
 Seq. ID LIB3431-062-P1-K1-C7
 Method BLASTX
 NCBI GI g4972111
 BLAST score 546
 E value 6.0e-56
 Match length 151
 % identity 62
 NCBI Description (AL078579) protein phosphatase homolog (PPH1) [Arabidopsis thaliana]

Seq. No. 403305
 Seq. ID LIB3431-062-P1-K1-C9
 Method BLASTN
 NCBI GI g2072554
 BLAST score 188
 E value 1.0e-101
 Match length 196
 % identity 99

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 403306
Seq. ID LIB3431-062-P1-K1-D1
Method BLASTN
NCBI GI g2267594
BLAST score 49
E value 4.0e-19
Match length 49
% identity 100

NCBI Description Oryza sativa plastocyanin precursor, mRNA, complete cds

Seq. No. 403307
Seq. ID LIB3431-062-P1-K1-D11
Method BLASTX
NCBI GI g1835731
BLAST score 461
E value 5.0e-46
Match length 95
% identity 95

NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 403308
Seq. ID LIB3431-062-P1-K1-D12
Method BLASTX
NCBI GI g2244965
BLAST score 307
E value 3.0e-28
Match length 85
% identity 68

NCBI Description (Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 403309
Seq. ID LIB3431-062-P1-K1-D2
Method BLASTN
NCBI GI g6015437
BLAST score 35
E value 3.0e-10
Match length 35
% identity 100

NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 403310
Seq. ID LIB3431-062-P1-K1-D3
Method BLASTX
NCBI GI g21695
BLAST score 361
E value 3.0e-34
Match length 110
% identity 62

NCBI Description (X66014) cathepsin B [Triticum aestivum]

Seq. No. 403311
Seq. ID LIB3431-062-P1-K1-D4
Method BLASTX
NCBI GI g4585882

BLAST score 444
E value 2.0e-45
Match length 141
% identity 70
NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein
[Arabidopsis thaliana]

Seq. No. 403312
Seq. ID LIB3431-062-P1-K1-D5
Method BLASTX
NCBI GI g3290022
BLAST score 434
E value 9.0e-43
Match length 142
% identity 58
NCBI Description (AF044173) cysteine synthase; CS-B; O-acetylserine (thiol)
lyase; plastidic isoform [Solanum tuberosum]

Seq. No. 403313
Seq. ID LIB3431-062-P1-K1-D7
Method BLASTX
NCBI GI g3201969
BLAST score 225
E value 2.0e-18
Match length 43
% identity 98
NCBI Description (AF068332) submergence induced protein 2A [Oryza sativa]

Seq. No. 403314
Seq. ID LIB3431-062-P1-K1-E1
Method BLASTN
NCBI GI g2624325
BLAST score 86
E value 9.0e-41
Match length 110
% identity 95
NCBI Description Oryza sativa mRNA for glycine-rich RNA-binding protein
(OsGRP1)

Seq. No. 403315
Seq. ID LIB3431-062-P1-K1-E11
Method BLASTN
NCBI GI g218209
BLAST score 155
E value 1.0e-81
Match length 281
% identity 96
NCBI Description Oryza sativa mRNA for the small subunit of
ribulose-1,5-bisphosphate carboxylase, complete cds, clone
pOSSS2106

Seq. No. 403316
Seq. ID LIB3431-062-P1-K1-E12
Method BLASTX
NCBI GI g3618310
BLAST score 331
E value 6.0e-31

000101-9T043960

Match length	109
% identity	46
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]
Seq. No.	403322
Seq. ID	LIB3431-062-P1-K1-E8
Method	BLASTN
NCBI GI	g5042437
BLAST score	287
E value	1.0e-160
Match length	358
% identity	99
NCBI Description	Oryza sativa BAC T49B20 genomic sequence, complete sequence
Seq. No.	403323
Seq. ID	LIB3431-062-P1-K1-F1
Method	BLASTX
NCBI GI	g4079798
BLAST score	227
E value	4.0e-20
Match length	92
% identity	60
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]
Seq. No.	403324
Seq. ID	LIB3431-062-P1-K1-F10
Method	BLASTX
NCBI GI	g132105
BLAST score	270
E value	4.0e-24
Match length	79
% identity	71
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]
Seq. No.	403325
Seq. ID	LIB3431-062-P1-K1-F11
Method	BLASTX
NCBI GI	g5042462
BLAST score	221
E value	9.0e-18
Match length	109
% identity	47
NCBI Description	(AC007789) putative negatively light-regulated protein [Oryza sativa]
Seq. No.	403326
Seq. ID	LIB3431-062-P1-K1-F12
Method	BLASTX

NCBI GI g2407281
 BLAST score 775
 E value 7.0e-83
 Match length 145
 % identity 99
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 403327
 Seq. ID LIB3431-062-P1-K1-F3
 Method BLASTX
 NCBI GI g3885894
 BLAST score 302
 E value 1.0e-27
 Match length 90
 % identity 72
 NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No. 403328
 Seq. ID LIB3431-062-P1-K1-F7
 Method BLASTX
 NCBI GI g3789952
 BLAST score 290
 E value 2.0e-26
 Match length 71
 % identity 86
 NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No. 403329
 Seq. ID LIB3431-062-P1-K1-F8
 Method BLASTX
 NCBI GI g2407281
 BLAST score 614
 E value 5.0e-64
 Match length 126
 % identity 90
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No. 403330
 Seq. ID LIB3431-062-P1-K1-F9
 Method BLASTX
 NCBI GI g132105
 BLAST score 391
 E value 7.0e-38
 Match length 108
 % identity 75
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 403331
 Seq. ID LIB3431-062-P1-K1-G1
 Method BLASTX
 NCBI GI g2462834
 BLAST score 293
 E value 3.0e-26
 Match length 106
 % identity 57
 NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 403332
 Seq. ID LIB3431-062-P1-K1-G10
 Method BLASTN
 NCBI GI g1835730
 BLAST score 156
 E value 1.0e-82
 Match length 164
 % identity 99
 NCBI Description Oryza sativa photosystem II 10 kDa polypeptide mRNA, complete cds

Seq. No. 403333
 Seq. ID LIB3431-062-P1-K1-G11
 Method BLASTX
 NCBI GI g3126854
 BLAST score 289
 E value 2.0e-26
 Match length 57
 % identity 98
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 403334
 Seq. ID LIB3431-062-P1-K1-G12
 Method BLASTX
 NCBI GI g3885892
 BLAST score 667
 E value 3.0e-70
 Match length 136
 % identity 94
 NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 403335
 Seq. ID LIB3431-062-P1-K1-G2
 Method BLASTX
 NCBI GI g5031281
 BLAST score 356
 E value 1.0e-33
 Match length 121
 % identity 60
 NCBI Description (AF139499) unknown [Prunus armeniaca]

Seq. No. 403336
 Seq. ID LIB3431-062-P1-K1-G3
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237


```
Seq. No.          403341
Seq. ID           LIB3431-062-P1-K1-G8
Method            BLASTN
NCBI GI           g20369
BLAST score       388
E value           0.0e+00
Match length      396
% identity        99
NCBI Description   Oryza sativa shoot GS2 mRNA for chloroplastic glutamine synthetase (EC 6.3.1.2) (clone lambda-GS31) >gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of chloroplast localising glutamine synthetase
```

```
Seq. No.          403342
Seq. ID           LIB3431-062-P1-K1-H2
Method            BLASTX
NCBI GI           g3289002
BLAST score       590
E value           4.0e-61
Match length      170
% identity        42
NCBI Description   (AF073522) CRP1 [Zea mays]
```

```
Seq. No.      403343
Seq. ID       LIB3431-062-P1-K1-H5
Method        BLASTX
NCBI GI       g2072555
BLAST score    237
E value       1.0e-19
Match length   44
% identity     100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
protein [Oryza sativa]
```

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Seq. No.          403344
Seq. ID           LIB3431-062-P1-K1-H7
Method            BLASTX
NCBI GI           g132105
BLAST score       606
E value           5.0e-63
Match length      131
% identity        87
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]

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```
Seq. No.      403345
Seq. ID      LIB3431-062-P1-K1-H9
Method       BLASTN
NCBI GI      q6015437
```


000101"91043950

BLAST score 162
E value 6.0e-86
Match length 282
% identity 89
NCBI Description Oryza sativa photosystem II 10 kDa polypeptide mRNA,
complete cds

Seq. No. 403351
Seq. ID LIB3431-062-P1-N1-A8
Method BLASTX
NCBI GI g2570513
BLAST score 172
E value 2.0e-12
Match length 32
% identity 97
NCBI Description (AF022739) chlorophyll a-b binding protein [Oryza sativa]

Seq. No. 403352
Seq. ID LIB3431-062-P1-N1-A9
Method BLASTX
NCBI GI g4138290
BLAST score 313
E value 1.0e-28
Match length 63
% identity 97
NCBI Description (AJ005841) thioredoxin M [Oryza sativa]

Seq. No. 403353
Seq. ID LIB3431-062-P1-N1-B1
Method BLASTX
NCBI GI g5931625
BLAST score 529
E value 6.0e-54
Match length 111
% identity 94
NCBI Description (AB032761) rab5B [Oryza sativa]

Seq. No. 403354
Seq. ID LIB3431-062-P1-N1-B10
Method BLASTX
NCBI GI g482311
BLAST score 398
E value 1.0e-38
Match length 79
% identity 100
NCBI Description photosystem II oxygen-evolving complex protein 1 - rice
(strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving
complex protein 1 [Oryza sativa]

Seq. No. 403355
Seq. ID LIB3431-062-P1-N1-B11
Method BLASTX
NCBI GI g3158476
BLAST score 166
E value 2.0e-11
Match length 43
% identity 70

000101-9T043950

NCBI Description (AF067185) aquaporin 2 [Samanea saman]

Seq. No. 403356
Seq. ID LIB3431-062-P1-N1-B12
Method BLASTX
NCBI GI g4914411
BLAST score 245
E value 1.0e-20
Match length 85
% identity 59

NCBI Description (AL050352) putative protein [Arabidopsis thaliana]

Seq. No. 403357
Seq. ID LIB3431-062-P1-N1-B3
Method BLASTX
NCBI GI g3108343
BLAST score 159
E value 1.0e-10
Match length 102
% identity 29

NCBI Description (AF061285) sesquiterpene cyclase [Capsicum annuum]

Seq. No. 403358
Seq. ID LIB3431-062-P1-N1-B4
Method BLASTX
NCBI GI g1261917
BLAST score 218
E value 2.0e-17
Match length 59
% identity 64

NCBI Description (X96979) lipid transfer protein 7a2b [Hordeum vulgare]

Seq. No. 403359
Seq. ID LIB3431-062-P1-N1-B5
Method BLASTX
NCBI GI g1617197
BLAST score 300
E value 3.0e-27
Match length 71
% identity 77

NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 403360
Seq. ID LIB3431-062-P1-N1-B7
Method BLASTX
NCBI GI g2286121
BLAST score 534
E value 1.0e-54
Match length 102
% identity 98

NCBI Description (U88068) sec14 like protein [Oryza sativa]

Seq. No. 403361
Seq. ID LIB3431-062-P1-N1-B8
Method BLASTN
NCBI GI g2305114
BLAST score 225

E value 1.0e-123
 Match length 352
 % identity 91
 NCBI Description Oryza sativa ferredoxin mRNA, complete cds

Seq. No. 403362
 Seq. ID LIB3431-062-P1-N1-B9
 Method BLASTX
 NCBI GI g132105
 BLAST score 411
 E value 4.0e-40
 Match length 76
 % identity 99
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 403363
 Seq. ID LIB3431-062-P1-N1-C11
 Method BLASTX
 NCBI GI g115787
 BLAST score 403
 E value 3.0e-39
 Match length 76
 % identity 100
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir_S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

Seq. No. 403364
 Seq. ID LIB3431-062-P1-N1-C12
 Method BLASTN
 NCBI GI g20262
 BLAST score 108
 E value 1.0e-53
 Match length 220
 % identity 87
 NCBI Description O.sativa light-induced mRNA

Seq. No. 403365
 Seq. ID LIB3431-062-P1-N1-C5
 Method BLASTN
 NCBI GI g218207
 BLAST score 256
 E value 1.0e-142
 Match length 284
 % identity 98
 NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone

pOSSS1139

Seq. No. 403366
 Seq. ID LIB3431-062-P1-N1-C6
 Method BLASTX
 NCBI GI g1854378
 BLAST score 275
 E value 4.0e-24
 Match length 60
 % identity 87
 NCBI Description (AB001338) Sucrose-Phosphate Synthase [Saccharum officinarum]

Seq. No. 403367
 Seq. ID LIB3431-062-P1-N1-C7
 Method BLASTX
 NCBI GI g3643090
 BLAST score 337
 E value 2.0e-31
 Match length 96
 % identity 66
 NCBI Description (AF075582) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]

Seq. No. 403368
 Seq. ID LIB3431-062-P1-N1-C8
 Method BLASTX
 NCBI GI g451193
 BLAST score 397
 E value 2.0e-38
 Match length 109
 % identity 72
 NCBI Description (L28008) wali7 [Triticum aestivum]
 >gi_1090845_prf__2019486B wali7 gene [Triticum aestivum]

Seq. No. 403369
 Seq. ID LIB3431-062-P1-N1-C9
 Method BLASTN
 NCBI GI g2072554
 BLAST score 317
 E value 1.0e-178
 Match length 325
 % identity 99
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 403370
 Seq. ID LIB3431-062-P1-N1-D1
 Method BLASTN
 NCBI GI g2267594
 BLAST score 43
 E value 1.0e-15
 Match length 43
 % identity 100
 NCBI Description Oryza sativa plastocyanin precursor, mRNA, complete cds

Seq. No. 403371

Seq. ID LIB3431-062-P1-N1-D11
 Method BLASTX
 NCBI GI g131400
 BLAST score 243
 E value 3.0e-27
 Match length 93
 % identity 67
 NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
 >gi_81471_pir_S00409 photosystem II 10K protein precursor
 - spinach >gi_170127 (J03887) 10kd polypeptide precursor
 [Spinacia oleracea]

Seq. No. 403372
 Seq. ID LIB3431-062-P1-N1-D12
 Method BLASTX
 NCBI GI g2244965
 BLAST score 157
 E value 2.0e-10
 Match length 37
 % identity 81
 NCBI Description (Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 403373
 Seq. ID LIB3431-062-P1-N1-D3
 Method BLASTN
 NCBI GI g21692
 BLAST score 43
 E value 9.0e-15
 Match length 75
 % identity 89
 NCBI Description T.aestivum mRNA 1 for cathepsin B (2529)

Seq. No. 403374
 Seq. ID LIB3431-062-P1-N1-D4
 Method BLASTX
 NCBI GI g115813
 BLAST score 280
 E value 8.0e-25
 Match length 68
 % identity 82
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
 CAB-8) >gi_19182_emb_CAA33330 (X15258) Type III
 chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 403375
 Seq. ID LIB3431-062-P1-N1-D5
 Method BLASTX
 NCBI GI g399333
 BLAST score 289
 E value 8.0e-26
 Match length 66
 % identity 88
 NCBI Description CYSTEINE SYNTHASE, CHLOROPLAST PRECURSOR (O-ACETYL SERINE
 SULFHYDRYLASE) (O-ACETYL SERINE (THIOL)-LYASE) (CSASE)
 >gi_322740_pir_A43407 cysteine synthase (EC 4.2.99.8)
 precursor - pepper >gi_17944_emb_CAA46086 (X64874)
 O-acetylserine (thiol)-lyase [Capsicum annuum]

Seq. No. 403386
 Seq. ID LIB3431-062-P1-N1-E8
 Method BLASTN
 NCBI GI g5042437
 BLAST score 283
 E value 1.0e-158
 Match length 342
 % identity 100
 NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence

Seq. No. 403387
 Seq. ID LIB3431-062-P1-N1-F1
 Method BLASTX
 NCBI GI g4079798
 BLAST score 455
 E value 3.0e-45
 Match length 88
 % identity 100
 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No. 403388
 Seq. ID LIB3431-062-P1-N1-F12
 Method BLASTX
 NCBI GI g347451
 BLAST score 154
 E value 4.0e-10
 Match length 29
 % identity 100
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 403389
 Seq. ID LIB3431-062-P1-N1-F3
 Method BLASTX
 NCBI GI g3885894
 BLAST score 330
 E value 1.0e-30
 Match length 77
 % identity 83
 NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No. 403390
 Seq. ID LIB3431-062-P1-N1-F6
 Method BLASTX
 NCBI GI g2997591
 BLAST score 306
 E value 8.0e-28
 Match length 74
 % identity 80
 NCBI Description (AF020814) glucose-6-phosphate/phosphate-translocator precursor [Pisum sativum]

Seq. No. 403391
 Seq. ID LIB3431-062-P1-N1-F7
 Method BLASTX
 NCBI GI g3789952

```
BLAST score      193
E value         1.0e-14
Match length    35
% identity      100
NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza
sativa]
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```
Seq. No.      203392
Seq. ID      LIB3431-062-P1-N1-F9
Method       BLASTX
NCBI GI      g132105
BLAST score   556
E value      3.0e-57
Match length  101
% identity    100
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                (D00643) small subunit of ribulose-1,5-bisphosphate
                carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364).
                ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                carboxylase S [Oryza sativa]
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```
Seq. No.          403393
Seq. ID           LIB3431-062-P1-N1-G1
Method            BLASTX
NCBI GI           g2462834
BLAST score       244
E value           1.0e-20
Match length      107
% identity        48
NCBI Description   (AF000657) hypothetical protein [Arabidopsis thaliana]
```

```
Seq. No.      403394
Seq. ID      LIB3431-062-P1-N1-G10
Method       BLASTX
NCBI GI      g1835731
BLAST score   426
E value      6.0e-42
Match length  92
% identity    89
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
```

```
Seq. No.      403395
Seq. ID      LIB3431-062-P1-N1-G11
Method       BLASTX
NCBI GI      g3126854
BLAST score   370
E value      2.0e-35
Match length  70
% identity   100
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```

Seq. No. 403396
Seq. ID LIB3431-062-P1-N1-G12

Method BLASTX
 NCBI GI g3885892
 BLAST score 208
 E value 1.0e-16
 Match length 41
 % identity 100
 NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 403397
 Seq. ID LIB3431-062-P1-N1-G2
 Method BLASTX
 NCBI GI g5031281
 BLAST score 223
 E value 4.0e-18
 Match length 47
 % identity 81
 NCBI Description (AF139499) unknown [Prunus armeniaca]

Seq. No. 403398
 Seq. ID LIB3431-062-P1-N1-G3
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 1.0e-19
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 403399
 Seq. ID LIB3431-062-P1-N1-G4
 Method BLASTX
 NCBI GI g5123711
 BLAST score 280
 E value 9.0e-25
 Match length 90
 % identity 61
 NCBI Description (AL079347) putative protein [Arabidopsis thaliana]

Seq. No. 403400
 Seq. ID LIB3431-062-P1-N1-G5
 Method BLASTX
 NCBI GI g347451
 BLAST score 220
 E value 9.0e-18
 Match length 65
 % identity 69
 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa]

Seq. No. 403401
 Seq. ID LIB3431-062-P1-N1-G6
 Method BLASTX
 NCBI GI g4973264
 BLAST score 376
 E value 4.0e-36

09624015 "101000

Match length	93
% identity	73
NCBI Description	(AF144391) thioredoxin-like 5 [Arabidopsis thaliana]
Seq. No.	403402
Seq. ID	LIB3431-062-P1-N1-G7
Method	BLASTX
NCBI GI	g2407279
BLAST score	206
E value	4.0e-16
Match length	42
% identity	100
NCBI Description	(AF017362) aldolase [Oryza sativa]
Seq. No.	403403
Seq. ID	LIB3431-062-P1-N1-G8
Method	BLASTN
NCBI GI	g20369
BLAST score	381
E value	0.0e+00
Match length	385
% identity	100
NCBI Description	Oryza sativa shoot GS2 mRNA for chloroplastic glutamine synthetase (EC 6.3.1.2) (clone lambda-GS31) >gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of chloroplast localising glutamine synthetase
Seq. No.	403404
Seq. ID	LIB3431-062-P1-N1-G9
Method	BLASTN
NCBI GI	g3885887
BLAST score	269
E value	1.0e-149
Match length	397
% identity	92
NCBI Description	Oryza sativa high mobility group protein (HMG) mRNA, complete cds
Seq. No.	403405
Seq. ID	LIB3431-062-P1-N1-H11
Method	BLASTX
NCBI GI	g451193
BLAST score	412
E value	3.0e-40
Match length	114
% identity	72
NCBI Description	(L28008) wali7 [Triticum aestivum] >gi_1090845_prf__2019486B wali7 gene [Triticum aestivum]
Seq. No.	403406
Seq. ID	LIB3431-062-P1-N1-H3
Method	BLASTX
NCBI GI	g3250697
BLAST score	377
E value	3.0e-36
Match length	91
% identity	76

NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 403407
 Seq. ID LIB3431-062-P1-N1-H5
 Method BLASTN
 NCBI GI g2072554
 BLAST score 285
 E value 1.0e-159
 Match length 301
 % identity 99
 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No. 403408
 Seq. ID LIB3431-062-P1-N1-H7
 Method BLASTX
 NCBI GI g132105
 BLAST score 402
 E value 4.0e-39
 Match length 73
 % identity 100
 NCBI Description RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 403409
 Seq. ID LIB3431-062-P1-N1-H9
 Method BLASTN
 NCBI GI g5051932
 BLAST score 200
 E value 1.0e-108
 Match length 254
 % identity 100
 NCBI Description Oryza sativa MADS-box protein FDRMADS8 mRNA, complete cds

Seq. No. 403410
 Seq. ID LIB3431-063-P1-K1-A1
 Method BLASTN
 NCBI GI g6015437
 BLAST score 41
 E value 1.0e-13
 Match length 41
 % identity 100
 NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 403411
 Seq. ID LIB3431-063-P1-K1-A11
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 7.0e-20

Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 403412
 Seq. ID LIB3431-063-P1-K1-A12
 Method BLASTX
 NCBI GI g3126854
 BLAST score 392
 E value 2.0e-38
 Match length 74
 % identity 100
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 403413
 Seq. ID LIB3431-063-P1-K1-A2
 Method BLASTX
 NCBI GI g132105
 BLAST score 363
 E value 1.0e-34
 Match length 101
 % identity 74
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 403414
 Seq. ID LIB3431-063-P1-K1-A3
 Method BLASTX
 NCBI GI g2407281
 BLAST score 696
 E value 1.0e-73
 Match length 144
 % identity 93
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
 subunit [Oryza sativa]

Seq. No. 403415
 Seq. ID LIB3431-063-P1-K1-A4
 Method BLASTN
 NCBI GI g3819202
 BLAST score 51
 E value 2.0e-19
 Match length 191
 % identity 82
 NCBI Description Hordeum vulgare partial mRNA; clone cMWG0680.rev

Seq. No. 403416
 Seq. ID LIB3431-063-P1-K1-A5

ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 403421
Seq. ID LIB3431-063-P1-K1-B10
Method BLASTX
NCBI GI g4220533
BLAST score 220
E value 2.0e-18
Match length 56
% identity 77
NCBI Description (AL035356) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No. 403422
Seq. ID LIB3431-063-P1-K1-B11
Method BLASTN
NCBI GI g6015437
BLAST score 38
E value 1.0e-12
Match length 38
% identity 100
NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 403423
Seq. ID LIB3431-063-P1-K1-B2
Method BLASTX
NCBI GI g3929924
BLAST score 479
E value 4.0e-48
Match length 93
% identity 98
NCBI Description (AB020502) catalase [Oryza sativa]

Seq. No. 403424
Seq. ID LIB3431-063-P1-K1-B3
Method BLASTX
NCBI GI g4103987
BLAST score 486
E value 6.0e-49
Match length 115
% identity 83
NCBI Description (AF030516) 5,10-methylenetetrahydrofolate dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase [Pisum sativum] >gi_6002383_emb_CAB56756.1 (AJ011589)
5,10-methylenetetrahydrofolate dehydrogenase:
5,10-methenyltetrahydrofolate cyclohydrolase [Pisum sativum]

Seq. No. 403425
Seq. ID LIB3431-063-P1-K1-B5
Method BLASTX
NCBI GI g2570511
BLAST score 256
E value 2.0e-22
Match length 57

Match length 77
 % identity 95
 NCBI Description *Oryza sativa* glycolate oxidase (GOX) mRNA, complete cds

Seq. No. 403436
 Seq. ID LIB3431-063-P1-K1-D10
 Method BLASTX
 NCBI GI g4038695
 BLAST score 198
 E value 3.0e-18
 Match length 63
 % identity 78
 NCBI Description (AB020945) ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit [*Avena sativa*]

Seq. No. 403437
 Seq. ID LIB3431-063-P1-K1-D11
 Method BLASTX
 NCBI GI g132105
 BLAST score 518
 E value 6.0e-53
 Match length 99
 % identity 95
 NCBI Description RUBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [*Oryza sativa*] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [*Oryza sativa*] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [*Oryza sativa*]

Seq. No. 403438
 Seq. ID LIB3431-063-P1-K1-D2
 Method BLASTX
 NCBI GI g5734636
 BLAST score 238
 E value 5.0e-20
 Match length 71
 % identity 56
 NCBI Description (AP000391) Similar to putative lipase (AC006232) [*Oryza sativa*]

Seq. No. 403439
 Seq. ID LIB3431-063-P1-K1-D5
 Method BLASTX
 NCBI GI g2407281
 BLAST score 159
 E value 3.0e-11
 Match length 39
 % identity 79
 NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [*Oryza sativa*]

Seq. No. 403440
 Seq. ID LIB3431-063-P1-K1-D6

Method BLASTN
 NCBI GI g218154
 BLAST score 39
 E value 4.0e-13
 Match length 59
 % identity 92
 NCBI Description Oryza sativa gene for cytoplasmic aldolase, complete cds,
 clone:Aldp.

Seq. No. 403457
 Seq. ID LIB3431-063-P1-K1-F9
 Method BLASTX
 NCBI GI g3126854
 BLAST score 388
 E value 1.0e-37
 Match length 82
 % identity 90
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 403458
 Seq. ID LIB3431-063-P1-K1-G1
 Method BLASTX
 NCBI GI g1184774
 BLAST score 502
 E value 8.0e-51
 Match length 114
 % identity 88
 NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
 GAPC3 [Zea mays]

Seq. No. 403459
 Seq. ID LIB3431-063-P1-K1-G12
 Method BLASTX
 NCBI GI g3913018
 BLAST score 698
 E value 7.0e-74
 Match length 139
 % identity 99
 NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
 (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic
 aldolase [Oryza sativa]

Seq. No. 403460
 Seq. ID LIB3431-063-P1-K1-G3
 Method BLASTN
 NCBI GI g11957
 BLAST score 342
 E value 0.0e+00
 Match length 362
 % identity 99
 NCBI Description Rice complete chloroplast genome

Seq. No. 403461
 Seq. ID LIB3431-063-P1-K1-G4
 Method BLASTX
 NCBI GI g3695005
 BLAST score 386

Seq. No. 403466
 Seq. ID LIB3431-063-P1-K1-H4
 Method BLASTX
 NCBI GI g3832512
 BLAST score 374
 E value 5.0e-36
 Match length 110
 % identity 69
 NCBI Description (AF097922) granule-bound glycogen (starch) synthase
 [Astragalus membranaceus]

Seq. No. 403467
 Seq. ID LIB3431-063-P1-K1-H5
 Method BLASTX
 NCBI GI g131225
 BLAST score 179
 E value 2.0e-13
 Match length 59
 % identity 66
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
 V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein
 precursor - barley >gi_167087 (M61146) photosystem I
 hydrophobic protein [Hordeum vulgare]

Seq. No. 403468
 Seq. ID LIB3431-063-P1-N1-A11
 Method BLASTX
 NCBI GI g2072555
 BLAST score 237
 E value 7.0e-20
 Match length 44
 % identity 100
 NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
 >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
 protein [Oryza sativa]

Seq. No. 403469
 Seq. ID LIB3431-063-P1-N1-A12
 Method BLASTX
 NCBI GI g3126854
 BLAST score 393
 E value 5.0e-38
 Match length 78
 % identity 95
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 403470
 Seq. ID LIB3431-063-P1-N1-A2
 Method BLASTX
 NCBI GI g132105
 BLAST score 508
 E value 2.0e-51
 Match length 91
 % identity 100
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

E value 4.0e-47
 Match length 89
 % identity 96
 NCBI Description LHCI-680, photosystem I antenna protein - barley
 >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
 antenna protein [Hordeum vulgare]

Seq. No. 403480
 Seq. ID LIB3431-063-P1-N1-B2
 Method BLASTX
 NCBI GI g3929924
 BLAST score 357
 E value 8.0e-34
 Match length 67
 % identity 99
 NCBI Description (AB020502) catalase [Oryza sativa]

Seq. No. 403481
 Seq. ID LIB3431-063-P1-N1-B3
 Method BLASTX
 NCBI GI g4103987
 BLAST score 486
 E value 6.0e-49
 Match length 115
 % identity 83
 NCBI Description (AF030516) 5,10-methylenetetrahydrofolate
 dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase
 [Pisum sativum] >gi_6002383_emb_CAB56756.1_ (AJ011589)
 5,10-methylenetetrahydrofolate dehydrogenase:
 5,10-methenyltetrahydrofolate cyclohydrolase [Pisum
 sativum]

Seq. No. 403482
 Seq. ID LIB3431-063-P1-N1-B5
 Method BLASTX
 NCBI GI g115793
 BLAST score 229
 E value 3.0e-23
 Match length 65
 % identity 91
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR
 (CAB) >gi_72749_pir_CDBH3 chlorophyll a/b-binding protein
 type III precursor - barley >gi_19023_emb_CAA44881_
 (X63197) type III LHCII CAB precursor protein [Hordeum
 vulgare]

Seq. No. 403483
 Seq. ID LIB3431-063-P1-N1-B8
 Method BLASTX
 NCBI GI g3126854
 BLAST score 410
 E value 4.0e-40
 Match length 78
 % identity 99
 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 403484

Seq. ID	LIB3431-063-P1-N1-B9
Method	BLASTN
NCBI GI	g5803242
BLAST score	388
E value	0.0e+00
Match length	484
% identity	100
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0535G04

```
Seq. No.      403485
Seq. ID       LIB3431-063-P1-N1-C12
Method        BLASTX
NCBI GI       g6103011
BLAST score    478
E value       5.0e-48
Match length  104
% identity    46
NCBI Description (X84225) precursor of photosystem II subunit (22KDa)
[Nicotiana tabacum]
```

```
Seq. No.          403486
Seq. ID           LIB3431-063-P1-N1-C3
Method            BLASTX
NCBI GI           g871931
BLAST score       220
E value           8.0e-18
Match length      59
% identity        71
NCBI Description   (D30763) ferredoxin [Oryza sativa]
```

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Seq. No.      403487
Seq. ID      LIB3431-063-P1-N1-C4
Method       BLASTX
NCBI GI      g132105
BLAST score   144
E value      5.0e-09
Match length  36
% identity    81
NCBI Description  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
```

```
Seq. No.      403488
Seq. ID.      LIB3431-063-P1-N1-C9
Method        BLASTX
NCBI GI       g4098250
BLAST score    164
E value       3.0e-11
Match length   71
% identity     41
NCBI Description (U76611) similar to Solanum tuberosum ci21A gene product
```



```

% identity      42
NCBI Description Z.mays complete chloroplast genome

Seq. No.        403494
Seq. ID         LIB3431-063-P1-N1-E4
Method          BLASTX
NCBI GI         g451193
BLAST score     314
E value         2.0e-33
Match length    120
% identity      68
NCBI Description (L28008) wali7 [Triticum aestivum]
>gi_1090845_prf__2019486B wali7 gene [Triticum aestivum]

Seq. No.        403495
Seq. ID         LIB3431-063-P1-N1-E5
Method          BLASTX
NCBI GI         g1835731
BLAST score     438
E value         2.0e-43
Match length    102
% identity      85
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.        403496
Seq. ID         LIB3431-063-P1-N1-E8
Method          BLASTN
NCBI GI         g2182028
BLAST score     324
E value         0.0e+00
Match length    324
% identity      100
NCBI Description Oryza sativa mRNA for shaggy-like kinase etha

Seq. No.        403497
Seq. ID         LIB3431-063-P1-N1-E9
Method          BLASTN
NCBI GI         g2331130
BLAST score     226
E value         1.0e-124
Match length    226
% identity      100
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
cds

Seq. No.        403498
Seq. ID         LIB3431-063-P1-N1-F10
Method          BLASTX
NCBI GI         g1705624
BLAST score     180
E value         4.0e-13
Match length    41
% identity      88
NCBI Description CATALASE ISOZYME A (CAT-A)

Seq. No.        403499
Seq. ID         LIB3431-063-P1-N1-F12

```


Match length 96
 % identity 95
 NCBI Description (AF017362) aldolase [Oryza sativa]

Seq. No. 403505
 Seq. ID LIB3431-063-P1-N1-F9
 Method BLASTX
 NCBI GI g115802
 BLAST score 189
 E value 3.0e-14
 Match length 36
 % identity 97
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I CAB-36) (LHCP) >gi_100311_pir_S21827 chlorophyll a/b-binding protein (cab-36) - common tobacco
 >gi_19827_emb_CAA41188_ (X58230) chlorophyll a/b binding protein [Nicotiana tabacum]

Seq. No. 403506
 Seq. ID LIB3431-063-P1-N1-G1
 Method BLASTX
 NCBI GI g120668
 BLAST score 469
 E value 7.0e-47
 Match length 102
 % identity 88
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
 >gi_82399_pir_A24159 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment)
 >gi_167044 (M36650) glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare] >gi_225347_prf_1301218A dehydrogenase, glyceraldehydephosphate [Hordeum vulgare var. distichum]

Seq. No. 403507
 Seq. ID LIB3431-063-P1-N1-G10
 Method BLASTX
 NCBI GI g21839
 BLAST score 595
 E value 7.0e-62
 Match length 118
 % identity 94
 NCBI Description (X57952) phosphoribulokinase [Triticum aestivum]

Seq. No. 403508
 Seq. ID LIB3431-063-P1-N1-G11
 Method BLASTX
 NCBI GI g517500
 BLAST score 273
 E value 3.0e-24
 Match length 68
 % identity 81
 NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf_1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No. 403509

Seq. ID LIB3431-063-P1-N1-G12
 Method BLASTX
 NCBI GI g2407279
 BLAST score 398
 E value 1.0e-38
 Match length 75
 % identity 100
 NCBI Description (AF017362) aldolase [Oryza sativa]

Seq. No. 403510
 Seq. ID LIB3431-063-P1-N1-G2
 Method BLASTX
 NCBI GI g4138290
 BLAST score 283
 E value 3.0e-25
 Match length 55
 % identity 100
 NCBI Description (AJ005841) thioredoxin M [Oryza sativa]

Seq. No. 403511
 Seq. ID LIB3431-063-P1-N1-G7
 Method BLASTX
 NCBI GI g2191138
 BLAST score 275
 E value 3.0e-24
 Match length 84
 % identity 64
 NCBI Description (AF007269) A_IG002N01.18 gene product [Arabidopsis thaliana]

Seq. No. 403512
 Seq. ID LIB3431-063-P1-N1-G8
 Method BLASTX
 NCBI GI g132105
 BLAST score 429
 E value 3.0e-42
 Match length 79
 % identity 99
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 403513
 Seq. ID LIB3431-063-P1-N1-H1
 Method BLASTX
 NCBI GI g693920
 BLAST score 419
 E value 5.0e-41
 Match length 80
 % identity 97
 NCBI Description (U21113) chlorophyll a/b binding protein [Solanum

050840Z 300700Z

```
Seq. No.          403517
Seq. ID           LIB3431-063-P1-N1-H5
Method            BLASTX
NCBI GI           g131225
BLAST score       216
E value           2.0e-17
Match length      56
% identity        73
```


37-kDa subunit from Homo sapiens and is a member of
PF_00004 ATPases associated with various cellular
activities. [Arabidopsis thaliana]

Seq. No. 403523
Seq. ID LIB3432-005-P1-K1-A3
Method BLASTX
NCBI GI g5912299
BLAST score 587
E value 7.0e-61
Match length 123
% identity 93
NCBI Description (AJ133787) gigantea homologue [Oryza sativa]

Seq. No. 403524
Seq. ID LIB3432-006-P1-K1-B8
Method BLASTX
NCBI GI g871931
BLAST score 492
E value 8.0e-50
Match length 116
% identity 88
NCBI Description (D30763) ferredoxin [Oryza sativa]

Seq. No. 403525
Seq. ID LIB3432-006-P1-K1-H9
Method BLASTX
NCBI GI g2827524
BLAST score 215
E value 2.0e-17
Match length 44
% identity 77
NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

Seq. No. 403526
Seq. ID LIB3432-007-P1-K1-B6
Method BLASTX
NCBI GI g1244566
BLAST score 719
E value 3.0e-76
Match length 145
% identity 92
NCBI Description (U39321) acetyl-CoA carboxylase [Triticum aestivum]
>gi_1588584_prf__2208491A Ac-CoA carboxylase [Triticum
aestivum]

Seq. No. 403527
Seq. ID LIB3432-007-P1-K1-C1
Method BLASTN
NCBI GI g577352
BLAST score 55
E value 6.0e-22
Match length 148
% identity 38
NCBI Description Streptococcus equi M protein (emmSzW60) gene, complete cds

Seq. No. 403528

Match length 44
 % identity 95
 NCBI Description (Y08962) transmembrane protein [Oryza sativa] >gi_1667594
 (U77297) transmembrane protein [Oryza sativa]

Seq. No. 403544
 Seq. ID LIB3432-012-P1-K1-D4
 Method BLASTX
 NCBI GI g4056490
 BLAST score 189
 E value 2.0e-14
 Match length 90
 % identity 42
 NCBI Description (AC005896) hypothetical protein [Arabidopsis thaliana]

Seq. No. 403545
 Seq. ID LIB3432-012-P1-K1-D7
 Method BLASTN
 NCBI GI g20155
 BLAST score 65
 E value 3.0e-28
 Match length 85
 % identity 94
 NCBI Description O.sativa random single-copy DNA fragment 12RG214R

Seq. No. 403546
 Seq. ID LIB3432-012-P1-K1-F3
 Method BLASTX
 NCBI GI g4662632
 BLAST score 230
 E value 6.0e-19
 Match length 71
 % identity 68
 NCBI Description (AC007267) unknown protein [Arabidopsis thaliana]

Seq. No. 403547
 Seq. ID LIB3432-012-P1-K1-G7
 Method BLASTN
 NCBI GI g5257255
 BLAST score 83
 E value 1.0e-38
 Match length 168
 % identity 86
 NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07

Seq. No. 403548
 Seq. ID LIB3432-012-P1-K1-H11
 Method BLASTX
 NCBI GI g3885892
 BLAST score 262
 E value 1.0e-22
 Match length 67
 % identity 79
 NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 403549
 Seq. ID LIB3432-012-P1-K1-H7

Method	BLASTX
NCBI GI	g4455680
BLAST score	150
E value	4.0e-10
Match length	66
% identity	47
NCBI Description	(AL035472) putative prolyl tRNA synthetase [Mycobacterium leprae]

```
Seq. No.      403550
Seq. ID      LIB3432-013-P1-K1-H12
Method       BLASTX
NCBI GI      g2373403
BLAST score   157
E value      5.0e-11
Match length  42
% identity    67
NCBI Description (D85193) similar to the membrane protein RD28 [Arabidopsis thaliana]
```

```
Seq. No.      403551
Seq. ID      LIB3432-014-P1-K1-H6
Method       BLASTX
NCBI GI      g4006855
BLAST score   215
E value      2.0e-17
Match length  76
% identity    57
NCBI Description (Z99707) Cu2+-transporting ATPase-like protein [Arabidopsis thaliana]
```

```
Seq. No.      403552
Seq. ID      LIB3432-015-P1-K1-D5
Method       BLASTX
NCBI GI      g1173347
BLAST score   618
E value      1.0e-64
Match length  120
% identity    94
NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
               (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
               >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC
               3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
               (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
               aestivum]
```

Seq. No.	403553
Seq. ID	LIB3432-015-P1-K1-D6
Method	BLASTX
NCBI GI	g2281115
BLAST score	631
E value	6.0e-66
Match length	154
% identity	76
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No. 403564
 Seq. ID LIB3432-020-P1-K1-D4
 Method BLASTN
 NCBI GI g5852170
 BLAST score 108
 E value 7.0e-54
 Match length 179
 % identity 89
 NCBI Description Oryza sativa indica (GLA4) genomic DNA, chromosome 4, BAC clone: t17804

Seq. No. 403565
 Seq. ID LIB3432-020-P1-K1-D5
 Method BLASTX
 NCBI GI g1173347
 BLAST score 189
 E value 1.0e-14
 Match length 79
 % identity 54
 NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]

Seq. No. 403566
 Seq. ID LIB3432-021-P1-K1-A2
 Method BLASTN
 NCBI GI g6063530
 BLAST score 39
 E value 5.0e-13
 Match length 43
 % identity 98
 NCBI Description Oryza sativa genomic DNA, chromosome 3, clone: P0043E01

Seq. No. 403567
 Seq. ID LIB3432-021-P1-K1-A3
 Method BLASTX
 NCBI GI g6063542
 BLAST score 273
 E value 3.0e-24
 Match length 61
 % identity 85
 NCBI Description (AP000615) EST C74302 (E30840) corresponds to a region of the predicted gene.; similar to glyceraldehyde-3-phosphate dehydrogenase. (M64118) [Oryza sativa]

Seq. No. 403568
 Seq. ID LIB3432-021-P1-K1-A7
 Method BLASTX
 NCBI GI g115766
 BLAST score 316
 E value 1.0e-29
 Match length 71
 % identity 76

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
 (D00643) small subunit of ribulose-1,5-bisphosphate
 carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
 sativa] >gi_226375_prf_1508256A ribulose bisphosphate
 carboxylase S [Oryza sativa]

Seq. No. 403578
 Seq. ID LIB3432-028-P1-K1-G5
 Method BLASTX
 NCBI GI g729535
 BLAST score 160
 E value 9.0e-11
 Match length 78
 % identity 46
 NCBI Description FERREDOXIN-THIOREDOXIN REDUCTASE, CATALYTIC CHAIN PRECURSOR
 (FTR-C) (FERREDOXIN-THIOREDOXIN REDUCTASE SUBUNIT B)
 (FTR-B)

Seq. No. 403579
 Seq. ID LIB3432-028-P1-K1-H3
 Method BLASTX
 NCBI GI g1217967
 BLAST score 438
 E value 3.0e-43
 Match length 124
 % identity 72
 NCBI Description (X96431) high affinity sulphate transporter [Hordeum
 vulgare]

Seq. No. 403580
 Seq. ID LIB3432-029-P1-K1-E3
 Method BLASTN
 NCBI GI g5803242
 BLAST score 221
 E value 1.0e-121
 Match length 334
 % identity 97
 NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04

Seq. No. 403581
 Seq. ID LIB3432-030-P1-K1-A1
 Method BLASTN
 NCBI GI g1835730
 BLAST score 129
 E value 3.0e-66
 Match length 285
 % identity 88
 NCBI Description Oryza sativa photosystem II 10 kDa polypeptide mRNA,
 complete cds

Seq. No. 403582
 Seq. ID LIB3432-030-P1-K1-A11
 Method BLASTN
 NCBI GI g1835730

000001-91048950

Seq. ID LIB3432-034-P2-K1-H5
 Method BLASTX
 NCBI GI g5007084
 BLAST score 696
 E value 1.0e-73
 Match length 133
 % identity 98
 NCBI Description (AF155333) NADP-specific isocitrate dehydrogenase [Oryza sativa]

Seq. No. 403588
 Seq. ID LIB3432-034-P2-K1-H6
 Method BLASTX
 NCBI GI g4895183
 BLAST score 272
 E value 6.0e-24
 Match length 105
 % identity 49
 NCBI Description (AC007661) hypothetical protein [Arabidopsis thaliana]

Seq. No. 403589
 Seq. ID LIB3432-035-P2-K1-A2
 Method BLASTN
 NCBI GI g304219
 BLAST score 70
 E value 3.0e-31
 Match length 173
 % identity 86
 NCBI Description Hordeum vulgare chloroplast photosystem I PSK-I subunit mRNA, complete cds

Seq. No. 403590
 Seq. ID LIB3432-035-P2-K1-A3
 Method BLASTX
 NCBI GI g3913018
 BLAST score 819
 E value 6.0e-88
 Match length 163
 % identity 96
 NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]

Seq. No. 403591
 Seq. ID LIB3432-035-P2-K1-C7
 Method BLASTN
 NCBI GI g4959460
 BLAST score 35
 E value 2.0e-10
 Match length 35
 % identity 100
 NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No. 403592
 Seq. ID LIB3432-035-P2-K1-G6
 Method BLASTX
 NCBI GI g132081

BLAST score 167
 E value 3.0e-13
 Match length 73
 % identity 55
 NCBI Description (AJ006752) starch synthase, isoform V [Vigna unguiculata]

Seq. No. 403598
 Seq. ID LIB3432-037-P1-K1-E3
 Method BLASTX
 NCBI GI g4850330
 BLAST score 332
 E value 7.0e-31
 Match length 63
 % identity 100
 NCBI Description (AB027123) cytochrome c oxidase subunit 5c [Oryza sativa]

Seq. No. 403599
 Seq. ID LIB3432-037-P1-K1-F7
 Method BLASTX
 NCBI GI g2773154
 BLAST score 217
 E value 6.0e-18
 Match length 71
 % identity 62
 NCBI Description (AF039573) abscisic acid- and stress-inducible protein [Oryza sativa]

Seq. No. 403600
 Seq. ID LIB3432-039-P1-K1-A2
 Method BLASTX
 NCBI GI g3122572
 BLAST score 519
 E value 8.0e-53
 Match length 148
 % identity 67
 NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi_1084434_pir_S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial complex I subunit [Solanum tuberosum]

Seq. No. 403601
 Seq. ID LIB3432-039-P1-K1-G6
 Method BLASTX
 NCBI GI g5091509
 BLAST score 719
 E value 3.0e-76
 Match length 134
 % identity 100
 NCBI Description (AB023482) EST AU065533(C2174) corresponds to a region of the predicted gene.; Similar to Homo sapiens splicing factor Prp8 mRNA, complete cds.(AF092565) [Oryza sativa]

Seq. No. 403602
 Seq. ID LIB3432-039-P1-K1-H12
 Method BLASTN

Seq. ID LIB3432-042-P2-K1-A9
 Method BLASTX
 NCBI GI g2662310
 BLAST score 219
 E value 3.0e-18
 Match length 66
 % identity 67
 NCBI Description (AB009307) bpw1 [Hordeum vulgare]

Seq. No. 403613
 Seq. ID LIB3432-042-P2-K1-B2
 Method BLASTX
 NCBI GI g3643607
 BLAST score 260
 E value 8.0e-23
 Match length 62
 % identity 76
 NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. 403614
 Seq. ID LIB3432-042-P2-K1-B3
 Method BLASTX
 NCBI GI g2129675
 BLAST score 555
 E value 4.0e-57
 Match length 122
 % identity 89
 NCBI Description probable chlorophyll synthetase G4 - Arabidopsis thaliana
 >gi_972938 (U19382) putative chlorophyll synthetase
 [Arabidopsis thaliana] >gi_3068709 (AF049236) putative
 chlorophyll synthetase [Arabidopsis thaliana]

Seq. No. 403615
 Seq. ID LIB3432-042-P2-K1-B4
 Method BLASTN
 NCBI GI g167086
 BLAST score 52
 E value 2.0e-20
 Match length 148
 % identity 84
 NCBI Description Hordeum vulgare photosystem I protein (PSI-L) mRNA,
 complete cds

Seq. No. 403616
 Seq. ID LIB3432-042-P2-K1-B7
 Method BLASTX
 NCBI GI g82080
 BLAST score 200
 E value 7.0e-16
 Match length 72
 % identity 60
 NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
 >gi_226872_prf_1609235A chlorophyll a/b binding protein
 [Lycopersicon esculentum]

Seq. No. 403617
 Seq. ID LIB3432-042-P2-K1-C11

Seq. ID LIB3432-043-P1-K1-G3
 Method BLASTX
 NCBI GI g3582333
 BLAST score 147
 E value 7.0e-10
 Match length 57
 % identity 58
 NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No. 403641
 Seq. ID LIB3432-043-P1-K1-H12
 Method BLASTN
 NCBI GI g6063530
 BLAST score 402
 E value 0.0e+00
 Match length 414
 % identity 99
 NCBI Description Oryza sativa genomic DNA, chromosome 3, clone:P0043E01

Seq. No. 403642
 Seq. ID LIB3432-043-P1-K1-H6
 Method BLASTX
 NCBI GI g1929998
 BLAST score 333
 E value 3.0e-31
 Match length 89
 % identity 78
 NCBI Description (U77463) NADPH-dependent HC-toxin reductase [Hordeum vulgare]

Seq. No. 403643
 Seq. ID LIB3432-044-P1-K1-B8
 Method BLASTX
 NCBI GI g2570511
 BLAST score 280
 E value 6.0e-25
 Match length 110
 % identity 72
 NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No. 403644
 Seq. ID LIB3432-044-P1-K1-C2
 Method BLASTX
 NCBI GI g435942
 BLAST score 383
 E value 5.0e-37
 Match length 107
 % identity 71
 NCBI Description (U04295) DNA-binding factor of bZIP class [Oryza sativa]

Seq. No. 403645
 Seq. ID LIB3432-044-P1-K1-G1
 Method BLASTX
 NCBI GI g3885884
 BLAST score 371
 E value 1.0e-35
 Match length 103

```

% identity      73
NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No.       403646
Seq. ID        LIB3432-044-P1-K1-H1
Method         BLASTX
NCBI GI        g5912424
BLAST score    512
E value        5.0e-52
Match length   150
% identity     71
NCBI Description (AJ242970) BTF3b-like factor [Arabidopsis thaliana]

Seq. No.       403647
Seq. ID        LIB3432-045-P1-K1-A8
Method         BLASTX
NCBI GI        g3367536
BLAST score    296
E value        5.0e-27
Match length   77
% identity     77
NCBI Description (AC004392) Contains similarity to symbiosis-related like
protein F1N20.80 gi_2961343 from A. thaliana BAC
gb_AL022140. EST gb_T04695 comes from this gene.
[Arabidopsis thaliana]

Seq. No.       403648
Seq. ID        LIB3432-045-P1-K1-B1
Method         BLASTX
NCBI GI        g804973
BLAST score    147
E value        3.0e-09
Match length   48
% identity     62
NCBI Description (X81376) L-ascorbate peroxidase [Capsicum annuum]

Seq. No.       403649
Seq. ID        LIB3432-045-P1-K1-G2
Method         BLASTX
NCBI GI        g4056502
BLAST score    414
E value        1.0e-40
Match length   105
% identity     75
NCBI Description (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]

Seq. No.       403650
Seq. ID        LIB3432-045-P1-K1-G3
Method         BLASTX
NCBI GI        g2911358
BLAST score    521
E value        5.0e-53
Match length   142
% identity     70
NCBI Description (AF041043) NADPH HC toxin reductase [Zea mays]

Seq. No.       403651

```

Seq. ID LIB3432-046-P1-K1-F7
 Method BLASTX
 NCBI GI g132105
 BLAST score 749
 E value 9.0e-80
 Match length 159
 % identity 90
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 403652
 Seq. ID LIB3432-047-P2-K11-G6
 Method BLASTN
 NCBI GI g6103440
 BLAST score 246
 E value 1.0e-136
 Match length 277
 % identity 98
 NCBI Description Oryza sativa metallothionein-like protein (ML2) mRNA, complete cds

Seq. No. 403653
 Seq. ID LIB3432-048-P2-K1-D6
 Method BLASTX
 NCBI GI g4469011
 BLAST score 392
 E value 5.0e-38
 Match length 103
 % identity 74
 NCBI Description (AL035602) carbohydrate kinase-like protein [Arabidopsis thaliana]

Seq. No. 403654
 Seq. ID LIB3432-048-P2-K1-E3
 Method BLASTX
 NCBI GI g3786009
 BLAST score 401
 E value 3.0e-39
 Match length 103
 % identity 76
 NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No. 403655
 Seq. ID LIB3432-048-P2-K1-F12
 Method BLASTN
 NCBI GI g5670155
 BLAST score 58
 E value 3.0e-24
 Match length 58
 % identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 403661
Seq. ID LIB3432-050-P1-K1-A7
Method BLASTX
NCBI GI g4115379
BLAST score 254
E value 9.0e-22
Match length 116
% identity 45
NCBI Description (AC005967) putative carbonyl reductase [Arabidopsis
thaliana]

Seq. No. 403662
Seq. ID LIB3432-050-P1-K1-E3
Method BLASTX
NCBI GI g2754849
BLAST score 227
E value 3.0e-19
Match length 52
% identity 85
NCBI Description (AF039000) putative serine-glyoxylate aminotransferase
[Fritillaria agrestis]

Seq. No. 403663
Seq. ID LIB3432-051-P1-K1-A2
Method BLASTN
NCBI GI g4158220
BLAST score 45
E value 3.0e-16
Match length 49
% identity 98
NCBI Description Oryza sativa mRNA for reversibly glycosylated polypeptide

Seq. No. 403664
Seq. ID LIB3432-051-P1-K1-D1
Method BLASTX
NCBI GI g132105
BLAST score 168
E value 3.0e-12
Match length 50
% identity 68
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

E value 1.0e-62
 Match length 159
 % identity 72
 NCBI Description (AC003952) hypothetical protein [Arabidopsis thaliana]

Seq. No. 403676
 Seq. ID LIB3432-058-P1-K1-C10
 Method BLASTN
 NCBI GI g21843
 BLAST score 43
 E value 4.0e-15
 Match length 73
 % identity 90
 NCBI Description Wheat PsbO mRNA for 33kDa oxygen evolving protein of photosystem II

Seq. No. 403677
 Seq. ID LIB3432-058-P1-K1-G5
 Method BLASTX
 NCBI GI g1805654
 BLAST score 265
 E value 5.0e-23
 Match length 101
 % identity 49
 NCBI Description (X99972) calmodulin-stimulated calcium-ATPase [Brassica oleracea]

Seq. No. 403678
 Seq. ID LIB3432-058-P1-K1-G6
 Method BLASTX
 NCBI GI g2765081
 BLAST score 636
 E value 5.0e-71
 Match length 154
 % identity 84
 NCBI Description (Y10557) g5bf [Arabidopsis thaliana]

Seq. No. 403679
 Seq. ID LIB3432-058-P1-K1-H5
 Method BLASTX
 NCBI GI g548605
 BLAST score 401
 E value 2.0e-39
 Match length 90
 % identity 89
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
 >gi_539055_pir_A48527 photosystem I protein psaK precursor
 - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No. 403680
 Seq. ID LIB3432-059-P1-K1-A8
 Method BLASTX
 NCBI GI g3914466
 BLAST score 440
 E value 1.0e-43

0984016 101000

```
Seq. No.      403691
Seq. ID      LIB3432-060-P1-K1-H6
Method       BLASTX
NCBI GI      g3868756
BLAST score   509
E value      6.0e-52
Match length  95
% identity    95
NCBI Description (D86611) catalase [Oryza sativa]
```

Seq. No.	403692
Seq. ID	LIB3433-001-P1-K1-D5
Method	BLASTX
NCBI GI	g2739366
BLAST score	167
E value	6.0e-12
Match length	67
% identity	49
NCBI Description	(AC002505) SF16 like protein [Arabidopsis thaliana]

```
Seq. No.      403693
Seq. ID      LIB3433-001-P1-K1-D6
Method       BLASTN
NCBI GI      g1815625
BLAST score   75
E value      3.0e-34
Match length 135
% identity    89
NCBI Description  Oryza sativa metallothionein-like type 1 (OsMT-1) mRNA,
complete cds
```

```
Seq. No.      403694
Seq. ID       LIB3433-001-P1-K1-F12
Method        BLASTX
NCBI GI       g3540195
BLAST score    250
E value        2.0e-21
Match length   108
% identity     27
NCBI Description (AC004260) Unknown protein [Arabidopsis thaliana]
```

51946

Seq. ID LIB3433-006-Q6-K6-E1
 Method BLASTX
 NCBI GI g3660467
 BLAST score 341
 E value 5.0e-32
 Match length 89
 % identity 76
 NCBI Description (AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis thaliana]

Seq. No. 403717
 Seq. ID LIB3433-006-Q6-K6-E11
 Method BLASTX
 NCBI GI g2407287
 BLAST score 188
 E value 4.0e-14
 Match length 59
 % identity 64
 NCBI Description (AF017366) metallothionein-like protein [Oryza sativa]

Seq. No. 403718
 Seq. ID LIB3433-006-Q6-K6-E5
 Method BLASTX
 NCBI GI g21839
 BLAST score 469
 E value 4.0e-47
 Match length 108
 % identity 80
 NCBI Description (X57952) phosphoribulokinase [Triticum aestivum]

Seq. No. 403719
 Seq. ID LIB3433-006-Q6-K6-E6
 Method BLASTX
 NCBI GI g548770
 BLAST score 511
 E value 5.0e-52
 Match length 121
 % identity 83
 NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_481228_pir_S38359 ribosomal protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630) ribosomal protein L3 [Oryza sativa]

Seq. No. 403720
 Seq. ID LIB3433-006-Q6-K6-E7
 Method BLASTX
 NCBI GI g5042453
 BLAST score 646
 E value 1.0e-67
 Match length 126
 % identity 97
 NCBI Description (AC007789) putative pathogenesis related protein [Oryza sativa]

Seq. No. 403721
 Seq. ID LIB3433-006-Q6-K6-E9
 Method BLASTN
 NCBI GI g170784

000001-91043950

BLAST score 40
E value 4.0e-13
Match length 71
% identity 89
NCBI Description Wheat ubiquitin carrier protein (UBC1) mRNA, complete cds

Seq. No. 403722
Seq. ID LIB3433-006-Q6-K6-F3
Method BLASTX
NCBI GI g5360230
BLAST score 751
E value 4.0e-80
Match length 141
% identity 98
NCBI Description (AB015287) Ran [Oryza sativa]

Seq. No. 403723
Seq. ID LIB3433-006-Q6-K6-H4
Method BLASTN
NCBI GI g5803242
BLAST score 353
E value 0.0e+00
Match length 353
% identity 100
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04

Seq. No. 403724
Seq. ID LIB3433-007-Q6-K1-H5
Method BLASTN
NCBI GI g218140
BLAST score 74
E value 2.0e-33
Match length 274
% identity 88
NCBI Description Rice mRNA abundantly expressed at microspore stage

Seq. No. 403725
Seq. ID LIB3433-008-Q6-K1-A3
Method BLASTX
NCBI GI g3935169
BLAST score 170
E value 5.0e-12
Match length 69
% identity 59
NCBI Description (AC004557) F17L21.12 [Arabidopsis thaliana]

Seq. No. 403726
Seq. ID LIB3433-011-Q6-K1-A7
Method BLASTX
NCBI GI g3212879
BLAST score 611
E value 1.0e-63
Match length 141
% identity 79
NCBI Description (AC004005) putative ribosomal protein L7 [Arabidopsis thaliana]

```
Seq. No.      403727
Seq. ID      LIB3433-011-Q6-K1-C4
Method       BLASTX
NCBI GI      g1705735
BLAST score   403
E value      3.0e-39
Match length  79
% identity    96
NCBI Description  CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM 11 (CDPK 11)
                >gi_1362175_pir_S56651 probable calcium-dependent protein
                kinase (clone OSCPK11) - rice >gi_587500_emb_CAA57156_
                (X81393) calcium-dependent protein kinase [Oryza sativa]
```

```
Seq. No.      403728
Seq. ID      LIB3433-011-Q6-K1-F2
Method       BLASTX
NCBI GI      g4731316
BLAST score   187
E value      2.0e-14
Match length  49
% identity    76
NCBI Description (AF120093) elongation factor 1-alpha [Nicotiana tabacum]
```

```
Seq. No.          403729
Seq. ID           LIB3433-012-Q6-K1-A11
Method            BLASTN
NCBI GI           g3282393
BLAST score       313
E value           1.0e-176
Match length      395
% identity        95
NCBI Description   Oryza sativa aie2 mRNA, partial cds
```

```
Seq. No.      403730
Seq. ID      LIB3433-012-Q6-K1-B3
Method       BLASTX
NCBI GI      g3914557
BLAST score   176
E value      9.0e-13
Match length 36
% identity   100
NCBI Description RAS-RELATED PROTEIN RAB7 (POSSIBLE AOSPORY-ASSOCIATED
PROTEIN) >gi_1155265 (U40219) possible apospory-associated
protein [Pennisetum ciliare]
```

```
Seq. No.          403731
Seq. ID           LIB3433-013-Q6-K1-D11
Method            BLASTN
NCBI GI           g19052
BLAST score       51
E value           1.0e-19
Match length      111
% identity        87
NCBI Description   H.vulgare Myb1 gene
```

Seq. No.	403732
Seq. ID	LIB3433-014-Q6-K1-A2

09684015.101000

Match length 84
 % identity 49
 NCBI Description (U57640) Bowman-Birk type trypsin inhibitor [*Oryza sativa*]

Seq. No. 403738
 Seq. ID LIB3433-015-Q6-K1-B7
 Method BLASTX
 NCBI GI g4406810
 BLAST score 339
 E value 6.0e-32
 Match length 90
 % identity 64
 NCBI Description (AC006201) unknown protein [*Arabidopsis thaliana*]

Seq. No. 403739
 Seq. ID LIB3433-015-Q6-K1-B8
 Method BLASTX
 NCBI GI g2431769
 BLAST score 217
 E value 1.0e-17
 Match length 60
 % identity 73
 NCBI Description (U62752) acidic ribosomal protein Pla [*Zea mays*]

Seq. No. 403740
 Seq. ID LIB3433-015-Q6-K1-C10
 Method BLASTN
 NCBI GI g4097153
 BLAST score 63
 E value 7.0e-27
 Match length 107
 % identity 89
 NCBI Description *Oryza sativa* type 1 metallothionein-like (rgMT-1) gene, complete cds

Seq. No. 403741
 Seq. ID LIB3433-015-Q6-K1-C3
 Method BLASTX
 NCBI GI g4850330
 BLAST score 321
 E value 1.0e-29
 Match length 63
 % identity 97
 NCBI Description (AB027123) cytochrome c oxidase subunit 5c [*Oryza sativa*]

Seq. No. 403742
 Seq. ID LIB3433-015-Q6-K1-C6
 Method BLASTX
 NCBI GI g505136
 BLAST score 159
 E value 1.0e-12
 Match length 54
 % identity 76
 NCBI Description (D30794) ferredoxin [*Oryza sativa*]

Seq. No. 403743
 Seq. ID LIB3433-015-Q6-K1-D3

09584016-101000

BLAST score 211
E value 9.0e-17
Match length 112
% identity 38
NCBI Description (Z98974) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 403760
Seq. ID LIB3433-017-Q6-K1-H4
Method BLASTN
NCBI GI g6016845
BLAST score 60
E value 5.0e-25
Match length 83
% identity 93
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No. 403761
Seq. ID LIB3433-017-Q6-K1-H6
Method BLASTX
NCBI GI g121528
BLAST score 292
E value 7.0e-28
Match length 111
% identity 66
NCBI Description GOS9 PROTEIN >gi_100683_pir_S19115 GOS9 protein - rice
>gi_20242_emb_CAA36189_ (X51909) GOS9 [Oryza sativa]

Seq. No. 403762
Seq. ID LIB3433-018-Q6-K6-D4
Method BLASTX
NCBI GI g2429292
BLAST score 197
E value 3.0e-15
Match length 117
% identity 45
NCBI Description (AF014470) peroxidase [Oryza sativa]

Seq. No. 403763
Seq. ID LIB3433-018-Q6-K6-E4
Method BLASTX
NCBI GI g2493147
BLAST score 315
E value 4.0e-29
Match length 77
% identity 84
NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_857574
(U27098) H+-ATPase [Oryza sativa]

Seq. No. 403764
Seq. ID LIB3433-019-P1-K1-A8
Method BLASTX
NCBI GI g1076732
BLAST score 455
E value 2.0e-45
Match length 120
% identity 72
NCBI Description type-1 pathogenesis-related protein - barley


```
Seq. No.      403769
Seq. ID      LIB3433-020-P1-K1-E2
Method       BLASTX
NCBI GI      g4506745
BLAST score   287
E value      7.0e-26
Match length  97
% identity    59
NCBI Description  ribosomal protein S9 >gi_1173285_sp_P46781_RS9_HUMAN 40S
RIBOSOMAL PROTEIN S9 >gi_1362936_pir__S55917 ribosomal
protein S9 - human >gi_550023 (U14971) ribosomal protein S9
[Homo sapiens] >gi_1096943_prf__2113200F ribosomal protein
S9 [Homo sapiens]
```

```
Seq. No.      403770
Seq. ID      LIB3433-020-P1-K1-E4
Method       BLASTX
NCBI GI      g4033424
BLAST score   581
E value      4.0e-60
Match length  125
% identity    92
NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
                PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic
                pyrophosphatase [Zea mays]
```

```
Seq. No.      403771
Seq. ID      LIB3433-020-P1-K1-E8
Method       BLASTX
NCBI GI      g3122599
BLAST score   155
E value      4.0e-10
Match length  76
% identity    42
NCBI Description  PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (PNP/PMP OXIDASE)
                >gi_1653389_dbj_BAA18303_(D90913) pyridoxamine 5-phosphate
                oxidase [Synechocystis sp.]
```

```
Seq. No.      403772
Seq. ID      LIB3433-020-P1-K1-F4
Method       BLASTX
NCBI GI      g2407287
BLAST score   185
E value      9.0e-14
Match length  59
% identity    63
NCBI Description (AF017366) metallothionein-like protein [Oryza sativa]
```

```
Seq. No.      403773
Seq. ID      LIB3433-020-P1-K1-G10
Method       BLASTX
NCBI GI      g4678941
BLAST score   327
E value      8.0e-31
Match length  133
% identity    56
NCBI Description (AL049711) gamma response I protein [Arabidopsis thaliana]
```

Seq. No.	403774
Seq. ID	LIB3433-020-P1-K1-G2
Method	BLASTX
NCBI GI	g4895197
BLAST score	145
E value	6.0e-09
Match length	44
% identity	59
NCBI Description	(AC007661) hypothetical protein [Arabidopsis thaliana]

```
Seq. No.      403775
Seq. ID       LIB3433-020-P1-K1-G4
Method        BLASTX
NCBI GI       g129591
BLAST score   620
E value       1.0e-64
Match length  135
% identity    93
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_
                (X16099) phenylalanine ammonia-lyase [Oryza sativa]
```

```
Seq. No.      403776
Seq. ID      LIB3433-020-P1-K1-G6
Method       BLASTX
NCBI GI      g1888357
BLAST score   325
E value      5.0e-34
Match length  148
% identity    55
NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana]
               >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase
               precursor [Arabidopsis thaliana]
```

```
Seq. No.      403777
Seq. ID      LIB3433-021-P1-K1-C2
Method       BLASTX
NCBI GI      g3335375
BLAST score   521
E value      4.0e-53
Match length  141
% identity    71
NCBI Description (AC003028) putative amidase [Arabidopsis thaliana]
```

```
Seq. No.      403778
Seq. ID      LIB3433-021-P1-K1-C4
Method       BLASTX
NCBI GI      g4099408
BLAST score   478
E value      4.0e-48
Match length 116
% identity   80
NCBI Description (U86763) delta-type tonoplast intrinsic protein [Triticum aestivum]
```

Seq. No.	403779
Seq. ID	LIB3433-021-P1-K1-G12

09564016-101000

NCBI Description (Z99753) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 403816
Seq. ID LIB3433-032-P1-K1-A2
Method BLASTX
NCBI GI g5263319
BLAST score 167
E value 3.0e-12
Match length 67
% identity 49
NCBI Description (AC007727) ESTs gb_N96028, gb_F14286, gb_T20680, gb_F14443, gb_AA657300 and gb_N65244 come from this gene. [Arabidopsis thaliana]

Seq. No. 403817
Seq. ID LIB3433-032-P1-K1-E11
Method BLASTX
NCBI GI g2462834
BLAST score 207
E value 3.0e-16
Match length 95
% identity 44
NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 403818
Seq. ID LIB3433-032-P1-K1-G2
Method BLASTX
NCBI GI g459895
BLAST score 292
E value 1.0e-33
Match length 86
% identity 85
NCBI Description (L29418) sus1 gene product [Zea mays]

Seq. No. 403819
Seq. ID LIB3433-033-P1-K1-D5
Method BLASTN
NCBI GI g1808687
BLAST score 90
E value 1.0e-42
Match length 246
% identity 89
NCBI Description S.stapfianus pSD.13 mRNA

Seq. No. 403820
Seq. ID LIB3433-033-P1-K1-E5
Method BLASTX
NCBI GI g1332579
BLAST score 490
E value 3.0e-64
Match length 180
% identity 8
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 403821
Seq. ID LIB3433-033-P1-K1-E8
Method BLASTX

000101-101000

NCBI GI g1729971
BLAST score 668
E value 4.0e-70
Match length 149
% identity 87
NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
(AQUAPORIN-TIP) >gi_1076745_pir_S52004 gamma-Tip protein -
rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
sativa]

Seq. No. 403822
Seq. ID LIB3433-033-P1-K1-F10
Method BLASTX
NCBI GI g3935141
BLAST score 342
E value 6.0e-32
Match length 109
% identity 53
NCBI Description (AC005106) T25N20.5 [Arabidopsis thaliana]

Seq. No. 403823
Seq. ID LIB3433-033-P1-K1-F4
Method BLASTX
NCBI GI g2662310
BLAST score 521
E value 7.0e-53
Match length 106
% identity 94
NCBI Description (AB009307) bpw1 [Hordeum vulgare]

Seq. No. 403824
Seq. ID LIB3433-033-P1-K1-G6
Method BLASTX
NCBI GI g283008
BLAST score 922
E value 1.0e-100
Match length 185
% identity 94
NCBI Description sucrose synthase (EC 2.4.1.13) - rice
>gi_20366_emb_CAA46017_ (X64770) sucrose synthase [Oryza
sativa]

Seq. No. 403825
Seq. ID LIB3433-033-P1-K1-H10
Method BLASTX
NCBI GI g629858
BLAST score 580
E value 8.0e-60
Match length 129
% identity 87
NCBI Description protein kinase C inhibitor - maize

Seq. No. 403826
Seq. ID LIB3433-034-P1-K1-F7
Method BLASTX
NCBI GI g2118425
BLAST score 243

```
E value      2.0e-20
Match length 60
% identity   80
NCBI Description subtilisin/chymotrypsin inhibitor - maize
>gi_475253_emb_CAA55588_(X78988) proteinase inhibitor [Zea
mays] >gi_475922_emb_CAA49593_(X69972) proteinase
inhibitor [Zea mays] >gi_559538_emb_CAA57677_(X82187)
subtilin/chymotrypsin-like inhibitor [Zea mays]
```

```
Seq. No.          403827
Seq. ID           LIB3433-034-P1-K1-F9
Method            BLASTX
NCBI GI           g2811122
BLAST score       205
E value           5.0e-16
Match length      107
% identity        38
NCBI Description   (U87318) NaDC-2 [Xenopus laevis]
```

Seq. No.	403828
Seq. ID	LIB3433-035-P1-K1-A7
Method	BLASTN
NCBI GI	g2335198
BLAST score	66
E value	1.0e-28
Match length	122
% identity	88
NCBI Description	Oryza sativa clone RGCH8 chitinase gene, complete cds

```
Seq. No.          403829
Seq. ID           LIB3433-037-P1-K1-H7
Method            BLASTN
NCBI GI           g1212995
BLAST score       48
E value           5.0e-18
Match length      147
% identity        85
NCBI Description   H.vulgare mRNA for UDP-glucose pyrophosphorylase
```

Seq. No.	403830
Seq. ID	LIB3433-038-P1-K1-A7
Method	BLASTX
NCBI GI	g295355
BLAST score	154
E value	1.0e-10
Match length	62
% identity	50
NCBI Description	(L13653) peroxidase [Lycopersicon esculentum]

Seq. No.	403831
Seq. ID	LIB3433-038-P1-K1-C6
Method	BLASTX
NCBI GI	g1888357
BLAST score	243
E value	2.0e-20
Match length	97
% identity	56

000001-9104350

NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana]
>gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase
precursor [Arabidopsis thaliana]

Seq. No. 403832
Seq. ID LIB3433-038-P1-K1-G6
Method BLASTX
NCBI GI g170031
BLAST score 214
E value 3.0e-17
Match length 73
% identity 59
NCBI Description (M10594) nodulin 35 [Glycine max]

Seq. No. 403833
Seq. ID LIB3433-038-P1-K1-G8
Method BLASTX
NCBI GI g2832672
BLAST score 247
E value 5.0e-21
Match length 51
% identity 94
NCBI Description (AL021712) nifU-like protein [Arabidopsis thaliana]

Seq. No. 403834
Seq. ID LIB3433-039-P1-K1-E7
Method BLASTN
NCBI GI g5410347
BLAST score 92
E value 5.0e-44
Match length 383
% identity 87
NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence

Seq. No. 403835
Seq. ID LIB3433-040-P1-K1-A7
Method BLASTN
NCBI GI g2331130
BLAST score 62
E value 4.0e-26
Match length 94
% identity 91
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
cds

Seq. No. 403836
Seq. ID LIB3433-040-P1-K1-D7
Method BLASTX
NCBI GI g401138
BLAST score 187
E value 6.0e-14
Match length 105
% identity 46
NCBI Description SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)
>gi_418758_pir_S29242 sucrose synthase (EC 2.4.1.13) Ss1 -
barley >gi_19106_emb_CAA46701_ (X65871) sucrose synthase
[Hordeum vulgare]

```
Seq. No.          403837
Seq. ID          LIB3433-040-P1-K1-H12
Method           BLASTX
NCBI GI         g462195
BLAST score      437
E value         3.0e-43
Match length     98
% identity       87
NCBI Description  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
                  >gi_100682_pir_S21636 GOS2 protein - rice
                  >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
                  >gi_3789950 (AF094774) translation initiation factor [Oryza
                  sativa]
```

```
Seq. No.          403838
Seq. ID           LIB3433-042-P1-K1-D3
Method            BLASTN
NCBI GI           g2773153
BLAST score       158
E value           9.0e-84
Match length      193
% identity        96
NCBI Description   Oryza sativa abscisic acid- and stress-inducible protein
                   (Asr1) mRNA, complete cds
```

Seq. No.	403839
Seq. ID	LIB3433-042-P1-K1-H11
Method	BLASTN
NCBI GI	g786129
BLAST score	40
E value	4.0e-13
Match length	48
% identity	96
NCBI Description	Oryza sativa root-specific RCc2 mRNA, complete cds

```
Seq. No.          403840
Seq. ID          LIB3433-045-P1-K1-A3
Method          BLASTX
NCBI GI         g2130067
BLAST score      717
E value         5.0e-76
Match length     139
% identity       99
NCBI Description aspartate transaminase (EC 2.6.1.1), mitochondrial - rice
                 >gi_2696240_dbj_BAA23815.1_(D67043) aspartate
                 aminotransferase [Oryza sativa]
```

```
Seq. No.      403841
Seq. ID       LIB3433-045-P1-K1-B1
Method        BLASTX
NCBI GI       g2117620
BLAST score   177
E value       1.0e-12
Match length  160
% identity    31
NCBI Description peroxidase (EC 1.11.1.7) 1A - alfalfa
```

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>gi_971558_emb_CAA62225_ (X90692) peroxidase1A [Medicago sativa]

Seq. No. 403842
Seq. ID LIB3433-045-P1-K1-H6
Method BLASTX
NCBI GI g1076740
BLAST score 537
E value 9.0e-60
Match length 143
% identity 78
NCBI Description chitinase (EC 3.2.1.14) - rice >gi_407472_emb_CAA40107_ (X56787) chitinase [Oryza sativa] >gi_500616_dbj_BAA03750_ (D16222) endochitinase [Oryza sativa]
>gi_742301_prf__2009354A chitinase [Oryza sativa]

Seq. No. 403843
Seq. ID LIB3433-048-P1-K1-D4
Method BLASTN
NCBI GI g2062705
BLAST score 32
E value 4.0e-09
Match length 32
% identity 100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 403844
Seq. ID LIB3433-048-P1-K1-D6
Method BLASTX
NCBI GI g3273243
BLAST score 377
E value 1.0e-36
Match length 78
% identity 96
NCBI Description (AB004660) NLS receptor [Oryza sativa]
>gi_3273245_dbj_BAA31166_ (AB004814) NLS receptor [Oryza sativa]

Seq. No. 403845
Seq. ID LIB3433-048-P1-K1-E2
Method BLASTN
NCBI GI g1196834
BLAST score 42
E value 1.0e-14
Match length 42
% identity 100
NCBI Description Oryza sativa (clone 14b) osmotin protein (14b) gene, 3' complete cds

Seq. No. 403846
Seq. ID LIB3433-048-P1-K1-F6
Method BLASTN
NCBI GI g5777612
BLAST score 97
E value 4.0e-47
Match length 228
% identity 85

NCBI GI g2130073
 BLAST score 406
 E value 1.0e-39
 Match length 131
 % identity 67
 NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301) aldolase C-1 [Oryza sativa]

Seq. No. 403853
 Seq. ID LIB3433-052-P1-K1-C4
 Method BLASTX
 NCBI GI g1362010
 BLAST score 155
 E value 2.0e-10
 Match length 47
 % identity 35
 NCBI Description ubiquitin-like protein 9 - Arabidopsis thaliana

Seq. No. 403854
 Seq. ID LIB3433-052-P1-K1-G6
 Method BLASTX
 NCBI GI g4455210
 BLAST score 456
 E value 3.0e-51
 Match length 139
 % identity 73
 NCBI Description (AL035440) putative aspartate-tRNA ligase [Arabidopsis thaliana]

Seq. No. 403855
 Seq. ID LIB3433-053-P1-K1-A7
 Method BLASTN
 NCBI GI g2293567
 BLAST score 78
 E value 7.0e-36
 Match length 92
 % identity 98
 NCBI Description Oryza sativa HvB12D homolog mRNA, complete cds

Seq. No. 403856
 Seq. ID LIB3433-054-P1-K1-D2
 Method BLASTX
 NCBI GI g1173218
 BLAST score 505
 E value 3.0e-51
 Match length 110
 % identity 91
 NCBI Description 40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No. 403857
 Seq. ID LIB3433-055-P1-K1-A3
 Method BLASTX
 NCBI GI g730463

Seq. No. 403867
 Seq. ID LIB3433-056-P1-K1-G3
 Method BLASTX
 NCBI GI g1076732
 BLAST score 328
 E value 1.0e-30
 Match length 85
 % identity 68
 NCBI Description type-1 pathogenesis-related protein - barley
 >gi_732807_emb_CAA88618_ (Z48728) type-1
 pathogenesis-related protein [Hordeum vulgare]

Seq. No. 403868
 Seq. ID LIB3433-057-P1-K1-A2
 Method BLASTX
 NCBI GI g1184112
 BLAST score 216
 E value 5.0e-31
 Match length 97
 % identity 76
 NCBI Description (U46138) Zn-induced protein [Oryza sativa]

Seq. No. 403869
 Seq. ID LIB3433-057-P1-K1-H6
 Method BLASTX
 NCBI GI g3123244
 BLAST score 188
 E value 3.0e-15
 Match length 132
 % identity 41
 NCBI Description ALPHA-MANNOSIDASE IIX (MANNOSYL-OLIGOSACCHARIDE
 1,3-1,6-ALPHA-MANNOSIDASE) (MAN IIX)
 >gi_1132479_dbj_BAA09510_ (D55649) alpha mannosidase II
 isozyme [Homo sapiens]

Seq. No. 403870
 Seq. ID LIB3433-058-P1-K1-B9
 Method BLASTN
 NCBI GI g809513
 BLAST score 79
 E value 2.0e-36
 Match length 154
 % identity 88
 NCBI Description Rice mRNA for ferredoxin-nitrite reductase, complete cds

Seq. No. 403871
 Seq. ID LIB3433-058-P1-K1-C1
 Method BLASTX
 NCBI GI g2341025
 BLAST score 221
 E value 7.0e-18
 Match length 63
 % identity 68
 NCBI Description (AC000104) F19P19.2 [Arabidopsis thaliana]

Seq. No. 403872

Seq. ID LIB3433-058-P1-K1-H12
 Method BLASTX
 NCBI GI g1076289
 BLAST score 254
 E value 2.0e-22
 Match length 69
 % identity 57
 NCBI Description amino acid permease AAP5 - Arabidopsis thaliana
 >gi_608673_emb_CAA54632_ (X77501) amino acid permease
 [Arabidopsis thaliana]

Seq. No. 403873
 Seq. ID LIB3433-061-P1-K1-A7
 Method BLASTX
 NCBI GI g4884530
 BLAST score 542
 E value 1.0e-55
 Match length 107
 % identity 98
 NCBI Description (AB027430) beta-1,3-glucanase [Oryza sativa]

Seq. No. 403874
 Seq. ID LIB3433-061-P1-K1-C10
 Method BLASTX
 NCBI GI g3695061
 BLAST score 232
 E value 8.0e-20
 Match length 56
 % identity 80
 NCBI Description (AF064788) rac GTPase activating protein 2 [Lotus japonicus]

Seq. No. 403875
 Seq. ID LIB3433-061-P1-K1-G5
 Method BLASTX
 NCBI GI g21693
 BLAST score 305
 E value 3.0e-28
 Match length 60
 % identity 83
 NCBI Description (X66012) cathepsin B [Triticum aestivum]

Seq. No. 403876
 Seq. ID LIB3433-061-P1-K1-H1
 Method BLASTX
 NCBI GI g2293480
 BLAST score 332
 E value 3.0e-31
 Match length 69
 % identity 91
 NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

Seq. No. 403877
 Seq. ID LIB3433-061-P1-K1-H12
 Method BLASTX
 NCBI GI g4388726
 BLAST score 492

% identity	81
NCBI Description	Oryza sativa COX5c mRNA for cytochrome c oxidase subunit 5c, complete cds
Seq. No.	403883
Seq. ID	LIB3434-003-P1-K1-A7
Method	BLASTX
NCBI GI	g3979986
BLAST score	253
E value	3.0e-22
Match length	52
% identity	96
NCBI Description	(Z98866) predicted using Genefinder; similar to Core histone H2A/H2B/H3/H4; cDNA EST EMBL:D71193 comes from this gene; cDNA EST yk477a9.3 comes from this gene; cDNA EST CEESG32RD comes from this gene; cDNA EST yk201g11.3 come
Seq. No.	403884
Seq. ID	LIB3434-003-P1-K1-C2
Method	BLASTX
NCBI GI	g5360230
BLAST score	578
E value	7.0e-60
Match length	106
% identity	99
NCBI Description	(AB015287) Ran [Oryza sativa]
Seq. No.	403885
Seq. ID	LIB3434-004-P1-K1-A2
Method	BLASTX
NCBI GI	g2293480
BLAST score	360
E value	7.0e-36
Match length	85
% identity	95
NCBI Description	(AF011331) glycine-rich protein [Oryza sativa]
Seq. No.	403886
Seq. ID	LIB3434-004-P1-K1-B1
Method	BLASTX
NCBI GI	g4567319
BLAST score	735
E value	5.0e-78
Match length	178
% identity	78
NCBI Description	(AC005956) putative copper amine oxidase [Arabidopsis thaliana]
Seq. No.	403887
Seq. ID	LIB3434-004-P1-K1-C4
Method	BLASTN
NCBI GI	g6016845
BLAST score	77
E value	4.0e-35
Match length	93
% identity	96
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

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Seq. No.          403899
Seq. ID           LIB3434-007-P1-K1-G2
Method            BLASTX
NCBI GI           g1729971
BLAST score       235
E value           7.0e-20
Match length      47
% identity        100
NCBI Description   TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                  (AQUAPORIN-TIP) >gi_1076745_pir_S52004 gamma-Tip protein -
                  rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
                  sativa]
```

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Seq. No.          403900
Seq. ID           LIB3434-007-P1-K1-H5
Method            BLASTX
NCBI GI           g2662310
BLAST score       391
E value           3.0e-41
Match length      97
% identity        90
NCBI Description   (AB009307) bpwl [Hordeum vulgare]
```

Seq. No.	403901
Seq. ID	LIB3434-008-P1-K1-A1
Method	BLASTN
NCBI GI	g2331130
BLAST score	39
E value	1.0e-12
Match length	75
% identity	89
NCBI Description	Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds

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E value 5.0e-32
 Match length 79
 % identity 81
 NCBI Description (Z49698) orf [Ricinus communis]

Seq. No. 403908
 Seq. ID LIB3434-009-P1-K1-H6
 Method BLASTX
 NCBI GI g6015742
 BLAST score 198
 E value 2.0e-15
 Match length 76
 % identity 51
 NCBI Description (Y18930) ribonuclease PH [Sulfolobus solfataricus]

Seq. No. 403909
 Seq. ID LIB3434-010-P1-K1-A12
 Method BLASTX
 NCBI GI g1805654
 BLAST score 556
 E value 4.0e-57
 Match length 165
 % identity 62
 NCBI Description (X99972) calmodulin-stimulated calcium-ATPase [Brassica oleracea]

Seq. No. 403910
 Seq. ID LIB3434-010-P1-K1-B4
 Method BLASTX
 NCBI GI g2935529
 BLAST score 663
 E value 1.0e-69
 Match length 150
 % identity 78
 NCBI Description (AF049069) No definition line found [Pinus radiata]

Seq. No. 403911
 Seq. ID LIB3434-010-P1-K1-D1
 Method BLASTN
 NCBI GI g303858
 BLAST score 209
 E value 1.0e-114
 Match length 217
 % identity 99
 NCBI Description Rice mRNA for brain specific protein (S94 gene), complete cds

Seq. No. 403912
 Seq. ID LIB3434-010-P1-K1-D8
 Method BLASTN
 NCBI GI g5688948
 BLAST score 115
 E value 5.0e-58
 Match length 183
 % identity 91
 NCBI Description Oryza sativa gene for mitochondrial ribosomal protein S14, succinate dehydrogenase iron-protein subunit (SDHB)

000101-97048960

Seq. No. 403913
Seq. ID LIB3434-010-P1-K1-H12
Method BLASTX
NCBI GI g3869088
BLAST score 603
E value 8.0e-63
Match length 117
% identity 98
NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No. 403914
Seq. ID LIB3434-011-P1-K1-A2
Method BLASTX
NCBI GI g3859116
BLAST score 337
E value 1.0e-31
Match length 106
% identity 72
NCBI Description (AF031609) unknown [Oryza sativa]

Seq. No. 403915
Seq. ID LIB3434-011-P1-K1-C4
Method BLASTX
NCBI GI g6056413
BLAST score 217
E value 1.0e-17
Match length 55
% identity 82
NCBI Description (AC009525) Unknown protein [Arabidopsis thaliana]

Seq. No. 403916
Seq. ID LIB3434-011-P1-K1-G6
Method BLASTN
NCBI GI g5929929
BLAST score 44
E value 1.0e-15
Match length 80
% identity 90
NCBI Description Zea mays voltage-dependent anion channel protein 1b
(vdac1b) mRNA, complete cds; nuclear gene for mitochondrial
product

Seq. No. 403917
Seq. ID LIB3434-012-P1-K1-A3
Method BLASTN
NCBI GI g5922603
BLAST score 201
E value 1.0e-109
Match length 220
% identity 99
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0705D01

Seq. No. 403918
Seq. ID LIB3434-012-P1-K1-E3
Method BLASTN
NCBI GI g2662344

Method	BLASTX
NCBI GI	g5081779
BLAST score	473
E value	1.0e-47
Match length	92
% identity	93
NCBI Description	(AF150630) cellulose synthase [Gossypium hirsutum]
Seq. No.	403930
Seq. ID	LIB3434-015-P1-K1-C1
Method	BLASTN
NCBI GI	g6016845
BLAST score	191
E value	1.0e-103
Match length	251
% identity	94
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
Seq. No.	403931
Seq. ID	LIB3434-015-P1-K1-D1
Method	BLASTX
NCBI GI	g1184774
BLAST score	692
E value	5.0e-73
Match length	157
% identity	85
NCBI Description	(U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]
Seq. No.	403932
Seq. ID	LIB3434-015-P1-K1-D6
Method	BLASTX
NCBI GI	g4544390
BLAST score	450
E value	1.0e-44
Match length	127
% identity	65
NCBI Description	(AC007047) hypothetical protein [Arabidopsis thaliana]
Seq. No.	403933
Seq. ID	LIB3434-015-P1-K1-E1
Method	BLASTX
NCBI GI	g5007084
BLAST score	908
E value	2.0e-98
Match length	172
% identity	98
NCBI Description	(AF155333) NADP-specific isocitrate dehydrogenase [Oryza sativa]
Seq. No.	403934
Seq. ID	LIB3434-015-P1-K1-G10
Method	BLASTX
NCBI GI	g2914706
BLAST score	707
E value	9.0e-75
Match length	159

000001-91048960

% identity 72
NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No. 403940
Seq. ID LIB3434-016-P1-K1-A11
Method BLASTN
NCBI GI g538427
BLAST score 274
E value 1.0e-152
Match length 285
% identity 99
NCBI Description Oryza sativa ribosomal protein S16 mRNA, complete cds

Seq. No. 403941
Seq. ID LIB3434-016-P1-K1-A2
Method BLASTX
NCBI GI g445613
BLAST score 353
E value 2.0e-33
Match length 97
% identity 70
NCBI Description ribosomal protein L7 [Solanum tuberosum]

Seq. No. 403942
Seq. ID LIB3434-016-P1-K1-A7
Method BLASTN
NCBI GI g167043
BLAST score 41
E value 1.0e-13
Match length 53
% identity 94
NCBI Description Barley glyceraldehyde-3-phosphate dehydrogenase mRNA, 3' end

Seq. No. 403943
Seq. ID LIB3434-016-P1-K1-C5
Method BLASTX
NCBI GI g1174162
BLAST score 406
E value 1.0e-39
Match length 88
% identity 80
NCBI Description (U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi_3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]

Seq. No. 403944
Seq. ID LIB3434-016-P1-K1-D4
Method BLASTX
NCBI GI g1705434
BLAST score 291
E value 3.0e-26
Match length 103
% identity 56
NCBI Description BIBENZYL SYNTHASE >gi_758243_emb_CAA56276_ (X79903) bibenzyl synthase [Phalaenopsis sp.]

00684016-101000

Seq. No. 403945
Seq. ID LIB3434-016-P1-K1-E2
Method BLASTX
NCBI GI g1710424
BLAST score 265
E value 6.0e-28
Match length 103
% identity 67
NCBI Description 50S RIBOSOMAL PROTEIN L21, CHLOROPLAST PRECURSOR (CL21)
>gi_2129718_pir_S71282 ribosomal protein L21 - Arabidopsis
thaliana >gi_1149573_emb_CAA89887_ (Z49787) chloroplast
ribosomal large subunit protein L21 [Arabidopsis thaliana]

Seq. No. 403946
Seq. ID LIB3434-016-P1-K1-F4
Method BLASTX
NCBI GI g2351580
BLAST score 596
E value 8.0e-62
Match length 134
% identity 82
NCBI Description (U82433) thymidine diphospho-glucose 4-6-dehydratase
homolog [Prunus armeniaca]

Seq. No. 403947
Seq. ID LIB3434-016-P1-K1-H5
Method BLASTX
NCBI GI g1519249
BLAST score 440
E value 5.0e-44
Match length 89
% identity 100
NCBI Description (U65956) GF14-b protein [Oryza sativa]

Seq. No. 403948
Seq. ID LIB3434-016-P1-K1-H6
Method BLASTX
NCBI GI g133867
BLAST score 438
E value 9.0e-48
Match length 114
% identity 82
NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir_S16577 ribosomal
protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)
ribosomal protein S11 [Zea mays]

Seq. No. 403949
Seq. ID LIB3434-017-P1-K1-A6
Method BLASTN
NCBI GI g4835773
BLAST score 36
E value 1.0e-10
Match length 68
% identity 88
NCBI Description Arabidopsis thaliana chromosome 1 BAC T16B5 sequence,
complete sequence

